

PCT

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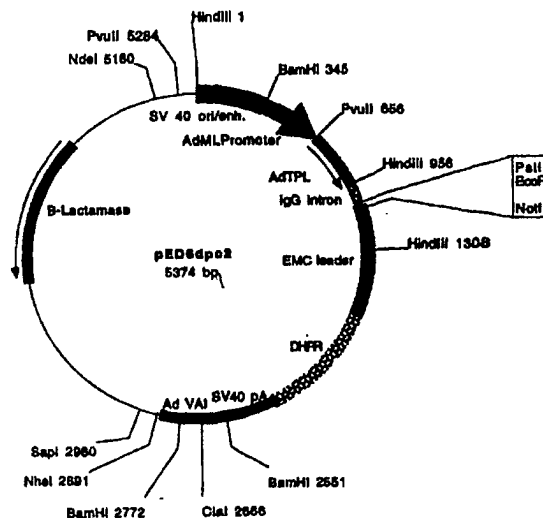
INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/47, A61K 38/17		A3	(11) International Publication Number: WO 98/40404
			(43) International Publication Date: 17 September 1998 (17.09.98)
(21) International Application Number: PCT/US98/04601		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: 9 March 1998 (09.03.98)		Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(30) Priority Data: 08/815,381 11 March 1997 (11.03.97) US 09/036,321 6 March 1998 (06.03.98) US		(88) Date of publication of the international search report: 30 December 1998 (30.12.98)	
(71) Applicant: GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US).			
(72) Inventors: JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). MCCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LAVALLIE, Edward, R.; 90 Green Meadow Drive, Tewksbury, MA 01876 (US). RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 93 Walcott Road, Chestnut Hill, MA 02167 (US). SPAULDING, Vikki; 11 Meadowbank Road, Billerica, MA 01821 (US). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US).			
(74) Agent: SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US).			

(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

(57) Abstract

Novel polynucleotides and the proteins encoded thereby are disclosed.



Plasmid name: pED6dpc2
Plasmid size: 5374 bp

Comments/References: pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

AL

INTERNATIONAL SEARCH REPORT

Internal Application No

PCT/US 98/04601

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/12 C07K14/47 A61K38/17

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 97 07198 A (GENETICS INST) 27 February 1997 see the whole document ---	1-11
A	US 5 536 637 A (K. JACOBS) 16 July 1996 cited in the application see the whole document ---	1-11
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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

4 August 1998

Date of mailing of the international search report

03.11.1998

Name and mailing address of the ISA
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Mateo Rosell, A.M.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/04601

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Y. FUJIOKA ET AL.: "A novel membrane glycoprotein, SHPS-1, that binds the SH2-domain-containing protein tyrosine phosphatase SHP-2 in response to mitogens and cell adhesion" MOLECULAR AND CELLULAR BIOLOGY, vol. 16, no. 12, 1996, WASHINGTON, DC, US, pages 6887-6899, XP002072087 cited in the application see the whole document and specially Figure 4	1,13
P,X	--- DATABASE NUCLEOTIDE PROTEIN SEQUENCE, - 28 October 1997 HINXTON, GB, XP002072088 AC= AA625610 similar to WP:K10B2.1 CE02008 transducin beta-chain	1,11
P,X	--- DATABASE NUCLEOTIDE PROTEIN SEQUENCE, - 6 February 1998 HINXTON, GB, XP002072072 AC= AA778577 similar to human TR:P78324 SHPS-1	1,11
T	--- DATABASE NUCLEOTIDE PROTEIN SEQUENCE, - 15 March 1998 HINXTON, GB, XP002072089 AC= AA861049 similar to human TR:P78324 SHPS-1	1,11
T	--- DATABASE NUCLEOTIDE PROTEIN SEQUENCE, - 15 March 1998 XP002072090 AC= AA862667 similar to human TR:P78324 SHPS-1 -----	1,11

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/ 04601

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claim 12 is directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-13

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-13

Polynucleotide comprising the nucleotide sequence of SEQ.ID.N.1 and encoding a polypeptide of SEQ.ID.N.2.
Polynucleotide fragments, variants, homologues and gene thereof. Host cells transformed with said polynucleotide.
Protein comprising SEQ.ID.N.2 or fragments thereof.
Pharmaceutical compositions.

2. Claims: 14-16

As invention 1 but concerning SEQ.ID.N.3, 4 and 31

3. Claims: 17-19

As invention 1 but concerning SEQ.ID.N.5 and 6

4. Claims: 20-22

As invention 1 but concerning SEQ.ID.N.7 and 8

5. Claims: 23-25

As invention 1 but concerning SEQ.ID.N.9 and 10

6. Claims: 26-28

As invention 1 but concerning SEQ.ID.N.11 and 12

7. Claims: 29-31

As invention 1 but concerning SEQ.ID.N.13 and 14

8. Claims: 32-34

As invention 1 but concerning SEQ.ID.N.15 and 16

9. Claims: 35-37

As invention 1 but concerning SEQ.ID.N.17 and 18

10. Claims: 38-40

As invention 1 but concerning SEQ.ID.N.19 and 20

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/04601

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9707198 A	27-02-1997	US 5707829 A	13-01-1998
		AU 6712396 A	18-02-1997
		AU 6768596 A	12-03-1997
		EP 0839196 A	06-05-1998
		EP 0851875 A	08-07-1998
		WO 9704097 A	06-02-1997
US 5536637 A	16-07-1996	US 5712116 A	27-01-1998

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(21) International Application Number: PCT/US98/04601		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).
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(74) Agent: SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US).		

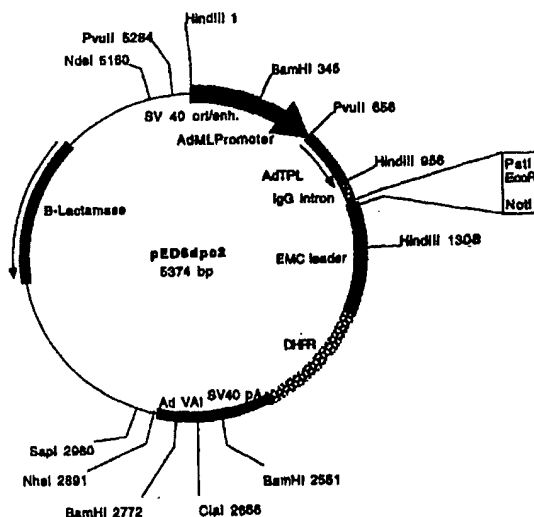
Published

Without international search report and to be republished upon receipt of that report.

(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

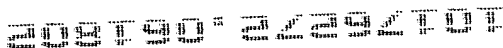
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Novel polynucleotides and the proteins encoded thereby are disclosed.



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Plasmid size: 5374 bp

Comments/References: pED8dpc2 is derived from pED8dpc1 by insertion of a new polylinker to facilitate cDNA cloning. 88T cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kautman et al.(1991), NAR 19: 4485-4490.



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SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

10 This application is a continuation-in-part of Ser. No. 60/XXX,XXX (converted to a provisional application from non-provisional application Ser. No. 08/815,381), filed March 11, 1997, which is incorporated by reference herein.

FIELD OF THE INVENTION

15 The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

BACKGROUND OF THE INVENTION

20 Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein

25 in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of

30 DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 521 to nucleotide 1111;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 536 to nucleotide 817;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ax318_3 deposited under accession number ATCC 98353;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ax318_3 deposited under accession number ATCC 98353;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone ax318_3 deposited under accession number ATCC 98353;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone ax318_3 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 93 to amino acid 102 of SEQ ID NO:2;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 521 to nucleotide 1111; the nucleotide sequence of SEQ ID NO:1 from nucleotide 536 to nucleotide 817; the nucleotide sequence of the full-length protein

coding sequence of clone ax318_3 deposited under accession number ATCC 98353; or the nucleotide sequence of the mature protein coding sequence of clone ax318_3 deposited under accession number ATCC 98353. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone ax318_3 deposited under accession number ATCC 98353. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2 from amino acid 4 to amino acid 99.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:2;
 - (b) the amino acid sequence of SEQ ID NO:2 from amino acid 4 to amino acid 99;
 - (c) fragments of the amino acid sequence of SEQ ID NO:2 comprising the amino acid sequence from amino acid 93 to amino acid 102 of SEQ ID NO:2; and
 - (d) the amino acid sequence encoded by the cDNA insert of clone ax318_3 deposited under accession number ATCC 98353;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2 or the amino acid sequence of SEQ ID NO:2 from amino acid 4 to amino acid 99.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 61 to nucleotide 864;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 826 to nucleotide 1386;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bg140_1 deposited under accession number ATCC 98353;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bg140_1 deposited under accession number ATCC 98353;

(f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone bg140_1 deposited under accession number ATCC 98353;

(g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone bg140_1 deposited under accession number ATCC 98353;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:4;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 61 to nucleotide 864; the nucleotide sequence of SEQ ID NO:3 from nucleotide 826 to nucleotide 1386; the nucleotide sequence of the full-length protein coding sequence of clone bg140_1 deposited under accession number ATCC 98353; or the nucleotide sequence of the mature protein coding sequence of clone bg140_1 deposited under accession number ATCC 98353. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone bg140_1 deposited under accession number ATCC 98353. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:31 from amino acid 148 to amino acid 249.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

SEQUENCE LISTING

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
- 5 (b) the amino acid sequence of SEQ ID NO:31;
- (c) the amino acid sequence of SEQ ID NO:31 from amino acid 148 to amino acid 249;
- (d) fragments of the amino acid sequence of SEQ ID NO:4 comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:4;
- 10 (e) fragments of the amino acid sequence of SEQ ID NO:31 comprising the amino acid sequence from amino acid 163 to amino acid 172 of SEQ ID NO:31; and
- (f) the amino acid sequence encoded by the cDNA insert of clone bg140_1 deposited under accession number ATCC 98353;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4, the amino acid sequence of SEQ ID NO:31, or the amino acid sequence of SEQ ID NO:31 from amino acid 148 to amino acid 249.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 77 to nucleotide 1624;
- 25 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 390 to nucleotide 789;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bg465_2 deposited under accession number ATCC 98353;
- 30 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bg465_2 deposited under accession number ATCC 98353;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone bg465_2 deposited under accession number ATCC 98353;

(g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone bg465_2 deposited under accession number ATCC 98353;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 253 to amino acid 262 of SEQ ID NO:6;

10 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

15 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 77 to nucleotide 1624; the nucleotide sequence of SEQ ID NO:5 from nucleotide 390 to nucleotide 789; the nucleotide sequence of the full-length protein coding sequence of clone bg465_2 deposited under accession number ATCC 98353; or the nucleotide sequence of the mature protein coding sequence of clone bg465_2 deposited
20 under accession number ATCC 98353. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone bg465_2 deposited under accession number ATCC 98353. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6 from amino acid 260 to amino acid
25 343.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
30 consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
- (b) the amino acid sequence of SEQ ID NO:6 from amino acid 260 to amino acid 343;

(c) fragments of the amino acid sequence of SEQ ID NO:6 comprising the amino acid sequence from amino acid 253 to amino acid 262 of SEQ ID NO:6; and

(d) the amino acid sequence encoded by the cDNA insert of clone bg465_2 deposited under accession number ATCC 98353; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6 or the amino acid sequence of SEQ ID NO:6 from amino acid 260 to amino acid 343.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 48 to nucleotide 1055;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 216 to nucleotide 1055;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 494 to nucleotide 958;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bk291_3 deposited under accession number ATCC 98353;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bk291_3 deposited under accession number ATCC 98353;
- (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone bk291_3 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone bk291_3 deposited under accession number ATCC 98353;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 85 to amino acid 94 of SEQ ID NO:8;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above; and

5 (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 48 to nucleotide 1055; the nucleotide sequence of SEQ ID NO:7 from nucleotide 216 to nucleotide 1055; the nucleotide sequence of SEQ ID NO:7 from
 10 nucleotide 494 to nucleotide 958; the nucleotide sequence of the full-length protein coding sequence of clone bk291_3 deposited under accession number ATCC 98353; or the nucleotide sequence of the mature protein coding sequence of clone bk291_3 deposited under accession number ATCC 98353. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of
 15 clone bk291_3 deposited under accession number ATCC 98353. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8 from amino acid 188 to amino acid 306.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
 20 ID NO:7.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
- 25 (b) the amino acid sequence of SEQ ID NO:8 from amino acid 188 to amino acid 306;
- (c) fragments of the amino acid sequence of SEQ ID NO:8 comprising the amino acid sequence from amino acid 85 to amino acid 94 of SEQ ID NO:8; and
- (d) the amino acid sequence encoded by the cDNA insert of clone
 30 bk291_3 deposited under accession number ATCC 98353;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8 or the amino acid sequence of SEQ ID NO:8 from amino acid 188 to amino acid 306.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 64 to nucleotide 1197;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 1 to nucleotide 828;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bp537_4 deposited under accession number ATCC 98353;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bp537_4 deposited under accession number ATCC 98353;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone bp537_4 deposited under accession number ATCC 98353;
- 15 (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone bp537_4 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- 20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:10;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).
- 30

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 64 to nucleotide 1197; the nucleotide sequence of SEQ ID NO:9 from nucleotide 1 to nucleotide 828; the nucleotide sequence of the full-length protein coding sequence of clone bp537_4 deposited under accession number ATCC 98353; or the

nucleotide sequence of the mature protein coding sequence of clone bp537_4 deposited under accession number ATCC 98353. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone bp537_4 deposited under accession number ATCC 98353. In yet other preferred
 5 embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10 from amino acid 1 to amino acid 255.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
 - (b) the amino acid sequence of SEQ ID NO:10 from amino acid 1 to
 15 amino acid 255;
 - (c) fragments of the amino acid sequence of SEQ ID NO:10 comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:10; and
 - (d) the amino acid sequence encoded by the cDNA insert of clone
 20 bp537_4 deposited under accession number ATCC 98353;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10 or the amino acid sequence of SEQ ID NO:10 from amino acid 1 to amino acid 255.

In one embodiment, the present invention provides a composition comprising an
 25 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 581 to nucleotide 1534;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
 30 NO:11 from nucleotide 928 to nucleotide 1510;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ts431_2 deposited under accession number ATCC 98353;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cs431_2 deposited under accession number ATCC 98353;

(f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone cs431_2 deposited under accession number ATCC 98353;

(g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone cs431_2 deposited under accession number ATCC 98353;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 154 to amino acid 163 of SEQ ID NO:12;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 581 to nucleotide 1534; the nucleotide sequence of SEQ ID NO:11 from nucleotide 928 to nucleotide 1510; the nucleotide sequence of the full-length protein coding sequence of clone cs431_2 deposited under accession number ATCC 98353; or the nucleotide sequence of the mature protein coding sequence of clone cs431_2 deposited under accession number ATCC 98353. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone cs431_2 deposited under accession number ATCC 98353. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12 from amino acid 150 to amino acid 310.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

SEQUENCE LISTING

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
- 5 (b) the amino acid sequence of SEQ ID NO:12 from amino acid 150 to amino acid 310;
- (c) fragments of the amino acid sequence of SEQ ID NO:12 comprising the amino acid sequence from amino acid 154 to amino acid 163 of SEQ ID NO:12; and
- 10 (d) the amino acid sequence encoded by the cDNA insert of clone cs431_2 deposited under accession number ATCC 98353;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12 or the amino acid sequence of SEQ ID NO:12 from amino acid 150 to amino acid 310.

- 15 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 29 to nucleotide 2227;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 1334 to nucleotide 2227;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 1 to nucleotide 746;
- 25 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw976_1 deposited under accession number ATCC 98353;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw976_1 deposited under accession number ATCC 98353;
- 30 (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone cw976_1 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone cw976_1 deposited under accession number ATCC 98353;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 361 to amino acid 370 of SEQ ID NO:14;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and

(m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 29 to nucleotide 2227; the nucleotide sequence of SEQ ID NO:13 from nucleotide 1334 to nucleotide 2227; the nucleotide sequence of SEQ ID NO:13 from nucleotide 1 to nucleotide 746; the nucleotide sequence of the full-length protein coding sequence of clone cw976_1 deposited under accession number ATCC 98353; or the nucleotide sequence of the mature protein coding sequence of clone cw976_1 deposited under accession number ATCC 98353. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone cw976_1 deposited under accession number ATCC 98353. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14 from amino acid 1 to amino acid 239, or a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14 from amino acid 119 to amino acid 733.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:14;

(b) the amino acid sequence of SEQ ID NO:14 from amino acid 1 to amino acid 239;

(c) the amino acid sequence of SEQ ID NO:14 from amino acid 119 to amino acid 733;

(d) fragments of the amino acid sequence of SEQ ID NO:14 comprising the amino acid sequence from amino acid 361 to amino acid 370 of SEQ ID NO:14;

5 and

(e) the amino acid sequence encoded by the cDNA insert of clone cw976_1 deposited under accession number ATCC 98353;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14, the amino acid sequence of SEQ ID NO:14 from amino acid 1 to amino acid 239, or the amino acid sequence of SEQ ID NO:14 from amino acid 119 to amino acid 733.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 364 to nucleotide 777;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 1 to nucleotide 636;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1233_3 deposited under accession number ATCC 98353;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1233_3 deposited under accession number ATCC 98353;

(f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone cw1233_3 deposited under accession number ATCC 98353;

(g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone cw1233_3 deposited under accession number ATCC 98353;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity; the fragment

comprising the amino acid sequence from amino acid 64 to amino acid 73 of SEQ ID NO:16;

(j) a polynucleotide which is an allelic variant of a polynucleotide of ~~SEQ ID NO:15~~ (a)-(g) above;

5 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
10 NO:15 from nucleotide 364 to nucleotide 777; the nucleotide sequence of SEQ ID NO:15 from nucleotide 1 to nucleotide 636; the nucleotide sequence of the full-length protein coding sequence of clone cw1233_3 deposited under accession number ATCC 98353; or the nucleotide sequence of the mature protein coding sequence of clone cw1233_3 deposited under accession number ATCC 98353. In other preferred embodiments, the
15 polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone cw1233_3 deposited under accession number ATCC 98353. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16 from amino acid 1 to amino acid 91.

20 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

25 (a) the amino acid sequence of SEQ ID NO:16;
(b) the amino acid sequence of SEQ ID NO:16 from amino acid 1 to amino acid 91;

(c) fragments of the amino acid sequence of SEQ ID NO:16 comprising the amino acid sequence from amino acid 64 to amino acid 73 of SEQ ID NO:16;
30 and

(d) the amino acid sequence encoded by the cDNA insert of clone cw1233_3 deposited under accession number ATCC 98353;

~~SEQ ID NO:15~~

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16 or the amino acid sequence of SEQ ID NO:16 from amino acid 1 to amino acid 91.

- 5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:
- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
 - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 619 to nucleotide 1434;
 - 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 520 to nucleotide 1323;
 - (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dg1_1 deposited under accession number ATCC 98353;
 - 15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dg1_1 deposited under accession number ATCC 98353;
 - (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone dg1_1 deposited under accession number ATCC 98353;
 - 20 (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone dg1_1 deposited under accession number ATCC 98353;
 - (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
 - (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 131 to amino acid 140 of SEQ ID NO:18;
 - 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
 - 30 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
 - (l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 619 to nucleotide 1434; the nucleotide sequence of SEQ ID NO:17 from nucleotide 520 to nucleotide 1323; the nucleotide sequence of the full-length protein coding sequence of clone dg1_1 deposited under accession number ATCC 98353; or the
 5 nucleotide sequence of the mature protein coding sequence of clone dg1_1 deposited under accession number ATCC 98353. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone dg1_1 deposited under accession number ATCC 98353. In yet other preferred
 10 embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18 from amino acid 1 to amino acid 235.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

In other embodiments, the present invention provides a composition comprising
 15 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
- (b) the amino acid sequence of SEQ ID NO:18 from amino acid 1 to amino acid 235;
- 20 (c) fragments of the amino acid sequence of SEQ ID NO:18 comprising the amino acid sequence from amino acid 131 to amino acid 140 of SEQ ID NO:18; and
- (d) the amino acid sequence encoded by the cDNA insert of clone dg1_1 deposited under accession number ATCC 98353;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:18 or the amino acid sequence of SEQ ID NO:18 from amino acid 1 to amino acid 235.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 2063 to nucleotide 2296.

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 2276 to nucleotide 2290;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 2037 to nucleotide 2405;
- 5 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ep234_1 deposited under accession number ATCC 98353;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ep234_1 deposited under accession number ATCC 98353;
- 10 (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone ep234_1 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone ep234_1 deposited under accession number ATCC 98353;
- 15 (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:20;
- 20 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- 25 (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 2063 to nucleotide 2290; the nucleotide sequence of SEQ ID NO:19 from nucleotide 2276 to nucleotide 2290; the nucleotide sequence of SEQ ID NO:19 from nucleotide 2037 to nucleotide 2405; the nucleotide sequence of the full-length protein coding sequence of clone ep234_1 deposited under accession number ATCC 98353; or the nucleotide sequence of the mature protein coding sequence of clone ep234_1 deposited under accession number ATCC 98353. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of

30

clone ep234_1 deposited under accession number ATCC 98353. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20 from amino acid 1 to amino acid 69.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:20;
- (b) the amino acid sequence of SEQ ID NO:20 from amino acid 1 to amino acid 69;
- (c) fragments of the amino acid sequence of SEQ ID NO:20 comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:20;
- 15 and
- (d) the amino acid sequence encoded by the cDNA insert of clone ep234_1 deposited under accession number ATCC 98353;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20 or the amino acid sequence of SEQ ID NO:20 from amino acid 1 to amino acid 69.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- 30 (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

DETAILED DESCRIPTION

ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Clone "ax318 3"

A polynucleotide of the present invention has been identified as clone "ax318_3". ax318_3 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ax318_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ax318_3 protein").

The nucleotide sequence of ax318_3 as presently determined is reported in SEQ ID NO:1. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ax318_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ax318_3 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for ax318_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ax318_3 demonstrated at least some similarity with sequences identified as AA255872 (zs19a01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone), AA625610 (zv89h04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 766999 3' similar to WP:K10B2.1 CE02008 TRANSDUCIN BETA CHAIN), D86043 (Human mRNA for SHPS-1, complete cds), H23217 (ym52f03.s1 Homo sapiens cDNA clone 51880 3'), U06701 (Human clone CCA53 mRNA containing CCA trinucleotide repeat), and W05822 (za90b02.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 299787 5'). The predicted amino acid sequence disclosed herein for ax318_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ax318_3 protein demonstrated at least some similarity to sequences identified as D85183 (SHPS-1 [Rattus rattus]), D86043 (SHPS-1 [Homo sapiens]), R85852 (WD-40 domain-containing beta-transducin protein), Y10376 (SIRP-beta1 [Homo sapiens]), and Z79757 (F55B12.3 [Caenorhabditis elegans]). SHPS-1 is a membrane glycoprotein that binds the SH2-domain-containing protein tyrosine phosphatase SHP-2 in response to mitogens and cell adhesion (Fujioka *et al.*, 1996, *Mol. Cell. Biol.* 16(12): 6887-6899, incorporated by reference herein). Based upon sequence similarity, ax318_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a putative transmembrane domain within the ax318_3 protein sequence, centered around amino acid 28 of SEQ ID NO:2; amino acids 15 to 27 of SEQ ID NO:2 are

also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28.

Clone "bg140_1"

5 A polynucleotide of the present invention has been identified as clone "bg140_1". bg140_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bg140_1 is a full-length clone,
10 including the entire coding sequence of a secreted protein (also referred to herein as "bg140_1 protein").

The nucleotide sequence of bg140_1 as presently determined is reported in SEQ ID NO:3. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bg140_1 protein corresponding to the foregoing
15 nucleotide sequence is reported in SEQ ID NO:4. Another possible bg140_1 reading frame and predicted amino acid sequence, encoded by base pairs 641 to 1648 of SEQ ID NO:3, is reported in SEQ ID NO:31. A frameshift in the nucleotide sequence of SEQ ID NO:3, caused, for example, by a single base pair deletion near position 825 of SEQ ID NO:3, could join the open reading frame encoding SEQ ID NO:4 with that encoding SEQ ID
20 NO:31.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bg140_1 should be approximately 2900 bp.

The nucleotide sequence disclosed herein for bg140_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. bg140_1 demonstrated at least some similarity with sequences identified as AA075629 (zm89a04.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 545070 3'), AA113989 (zn27h12.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 548711 5'), N77135 (yz85h11.r1 Homo sapiens cDNA clone 289893 5'), R11701 (yf49d02.r1 Homo sapiens cDNA clone 25600 5'), R13178
30 (yf73e04.r1 Homo sapiens cDNA clone 27855 5'), and Y14946 (Homo sapiens mRNA for SPIN protein). The predicted amino acid sequence disclosed herein for bg140_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bg140_1 protein demonstrated at least some similarity to sequences identified as AF038969 (general transcription factor 2-I [Homo

sapiens]), U77948 (Bruton's tyrosine kinase-associated protein-135; BAP-135 [Homo sapiens]), and Y14946 (SPIN protein [Homo sapiens]). Based upon sequence similarity, bg140_1 proteins and each similar protein or peptide may share at least some activity.

*** SEQUENCING IN PROGRESS ***

5 Clone "bg465_2"

A polynucleotide of the present invention has been identified as clone "bg465_2". bg465_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
10 analysis of the amino acid sequence of the encoded protein. bg465_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bg465_2 protein").

The nucleotide sequence of bg465_2 as presently determined is reported in SEQ ID NO:5. What applicants presently believe to be the proper reading frame and the
15 predicted amino acid sequence of the bg465_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bg465_2 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for bg465_2 was searched against the
20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bg465_2 demonstrated at least some similarity with sequences identified as AA133150 (zm25b07.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 526645 5' similar to WP:F07F6.4 CE01896 ZINC FINGER PROTEIN), AA144842 (mr69h01.r1 Stratagene mouse testis (#937308) Mus musculus cDNA clone 602737 5'),
25 AA484561 (nf06a12.s1 NCI_CGAP_Li1 Homo sapiens cDNA clone), D16939 (Human HepG2 3' region cDNA, clone hmd5d06), L24125 (Saccharomyces cerevisiae zinc finger protein (GCS1) gene, complete cds), R18422 (yg02f06.r1 Homo sapiens cDNA clone 30950 5'), T32543 (EST50558 Homo sapiens cDNA 5' end similar to None), W88569 (zh70b12.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417407 3'), Z74274
30 (S.cerevisiae chromosome IV reading frame ORF YDL226c), and Z82199 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5; HTGS phase 1). The predicted amino acid sequence disclosed herein for bg465_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bg465_2 protein demonstrated at least some similarity to sequences

identified as U23486 (similar to *S. cerevisiae* zinc finger protein GCS1 (SP GCS1_YEAST) [Caenorhabditis elegans]). Based upon sequence similarity, bg465_2 proteins and each similar protein or peptide may share at least some activity.

5 Clone "bk291 3"

A polynucleotide of the present invention has been identified as clone "bk291_3". bk291_3 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bk291_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bk291_3 protein").

The nucleotide sequence of bk291_3 as presently determined is reported in SEQ ID NO:7. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bk291_3 protein corresponding to the foregoing
15 nucleotide sequence is reported in SEQ ID NO:8. Amino acids 44 to 56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 57, or are a transmembrane domain.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
20 bk291_3 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for bk291_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bk291_3 demonstrated at least some similarity with sequences identified as AA135915 (zl19f04.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502399 5'), AA156738 (zl19f04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502399 3' similar to WP:T05E11.5 CE06364 YEAST YKK0 LIKE), AF017785 (Mus musculus MHC Class I H13a minor histocompatibility peptide (H13) mRNA, partial cds), N40134 (yw73a12.r1 Homo sapiens cDNA clone 257854 5' similar to SW:YKK0_YEAST P34248 HYPOTHETICAL 67.5 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION), N42726 (yy11d01.r1 Homo sapiens cDNA clone 270913 5' similar to SW:YKK0_YEAST P34248 HYPOTHETICAL 67.5 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION), R67144 (yi31h04.r1 Homo sapiens cDNA clone 140887 5' similar to SP:YKK0_YEAST P34248 HYPOTHETICAL 67.5 KD PROTEIN IN APE1/LAP4-MBR1 INTERGENIC), R78822 (yi90b05.r1 Homo sapiens cDNA clone 146481 5'), R79317

(yi90b05.s1 Homo sapiens cDNA clone 146481 3'), T23944 (Human gene signature HUMGS05889), and W04243 (za58h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone). The predicted amino acid sequence disclosed herein for bk291_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bk291_3 protein demonstrated at least some similarity to sequences identified as X71133 (YKL450 [Saccharomyces cerevisiae]), Z28100 (ORF YKL100c [Saccharomyces cerevisiae]), and Z68751 (T05E11.5 [Caenorhabditis elegans]). Based upon sequence similarity, bk291_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six additional potential transmembrane domains within the bk291_3 protein sequence, centered around amino acids 70, 125, 170, 220, 260, and 280 of SEQ ID NO:8.

Clone "bp537_4"

A polynucleotide of the present invention has been identified as clone "bp537_4". bp537_4 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bp537_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bp537_4 protein").

The nucleotide sequence of bp537_4 as presently determined is reported in SEQ ID NO:9. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bp537_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bp537_4 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for bp537_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bp537_4 demonstrated at least some similarity with sequences identified as AA007576 (zh99b06.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429395 5'), AA287563 (zs52g02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA 5'), R09093 (yf21h09.r1 Homo sapiens cDNA clone 127553 5'), and T33088 (EST56631 Homo sapiens cDNA 5' end similar to None). The predicted amino acid sequence disclosed herein for bp537_4 was searched against the GenPept and GeneSeq amino acid

sequence databases using the BLASTX search protocol. The predicted bp537_4 protein demonstrated at least some similarity to sequences identified as U34998 (Rad9 [Coprinus cinereus]). Based upon sequence similarity, bp537_4 proteins and each similar protein or peptide may share at least some activity.

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Clone "cs431_2"

A polynucleotide of the present invention has been identified as clone "cs431_2". cs431_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
10 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cs431_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cs431_2 protein").

The nucleotide sequence of cs431_2 as presently determined is reported in SEQ ID
15 NO:11. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cs431_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cs431_2 should be approximately 2300 bp.

20 The nucleotide sequence disclosed herein for cs431_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cs431_2 demonstrated at least some similarity with sequences identified as AA021033 (ze67h12.s1 Soares retina N2b4HR Homo sapiens cDNA clone 364103 3' similar to contains Alu repetitive element), H29349 (ym32c02.r1 Homo sapiens
25 cDNA clone 49839 5' similar to SP:KYES_XIPHE P27447 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES), L14577 (Homo sapiens cystathionine beta-synthase (CBS) mRNA, complete cds), Q87430 (Human cystathionine beta-synthase cDNA), and X92659 (H.sapiens intron 4 from p53 gene). The predicted amino acid sequence disclosed herein for cs431_2 was searched against the GenPept and GeneSeq amino acid sequence
30 databases using the BLASTX search protocol. The predicted cs431_2 protein demonstrated at least some similarity to sequences identified as L19501 (cystathionine beta-synthase [Homo sapiens]), R71376 (Human cystathionine beta-synthase), U61167 (SH3 domain-containing protein SH3P18 [Homo sapiens]), and X82166 (cystathionine beta-synthase [Homo sapiens]). Based upon sequence similarity, cs431_2 proteins and

each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cs431_2 protein sequence centered around amino acid 30 of SEQ ID NO:12. The nucleotide sequence of cs431_2 ~~indicates that it may contain an Alu repetitive element.~~

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Clone "cw976_1"

A polynucleotide of the present invention has been identified as clone "cw976_1". cw976_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
10 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw976_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw976_1 protein").

The nucleotide sequence of cw976_1 as presently determined is reported in SEQ
15 ID NO:13. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw976_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14. Amino acids 423 to 435 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 436, or are a transmembrane domain.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw976_1 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for cw976_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw976_1 demonstrated at least some similarity with sequences
25 identified as AA280747 (zs96a09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711448 5'), AA323946 (EST26798 Cerebellum II Homo sapiens cDNA 5' end), R13665 (yf60g06.r1 Homo sapiens cDNA clone 26764 5'), R16892 (yf44d06.s2 Homo sapiens cDNA clone 129707 3'), R85177 (yo43d07.r1 Homo sapiens cDNA clone 180685 5'), and R89648 (ym97c02.r1 Homo sapiens cDNA clone 166850 5'). Based upon sequence
30 similarity, cw976_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cw976_1 protein sequence at the amino terminus of SEQ ID NO:14.

~~indicates that it may contain an Alu repetitive element.~~

Clone "cw1233_3"

A polynucleotide of the present invention has been identified as clone "cw1233_3". cw1233_3 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
 5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw1233_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw1233_3 protein").

The nucleotide sequence of cw1233_3 as presently determined is reported in SEQ
 10 ID NO:15. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw1233_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1233_3 should be approximately 3000 bp.

15 The nucleotide sequence disclosed herein for cw1233_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1233_3 demonstrated at least some similarity with sequences identified as R61600 (yh16f08.r1 Homo sapiens cDNA clone 37807 5'), R83929 (yp06h11.s1 Homo sapiens cDNA clone 186693 3' similar to contains Alu repetitive element; contains
 20 TAR1 repetitive element), R87877 (yo45h05.r1 Homo sapiens cDNA clone 180921 5'), U14568 (**ALU WARNING Human Alu-Sb subfamily consensus sequence). The predicted amino acid sequence disclosed herein for cw1233_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1233_3 protein demonstrated at least some similarity to sequences
 25 identified as AB002317 (KIAA0319 [Homo sapiens]). Based upon sequence similarity, cw1233_3 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of cw1233_3 indicates that it may contain an Alu repetitive element.

30 Clone "dg1_1"

A polynucleotide of the present invention has been identified as clone "dg1_1". dg1_1 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
 identified as encoding a secreted or transmembrane protein on the basis of computer

analysis of the amino acid sequence of the encoded protein. dg1_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dg1_1 protein").

- 5 The nucleotide sequence of dg1_1 as presently determined is reported in SEQ ID NO:17. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dg1_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:18.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dg1_1 should be approximately 1900 bp.

- 10 The nucleotide sequence disclosed herein for dg1_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dg1_1 demonstrated at least some similarity with sequences identified as AA731281 (nw57f05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 1250721 similar to gb Y00345_cds1 POLYADENYLATE-BINDING PROTEIN (HUMAN)).
- 15 The predicted amino acid sequence disclosed herein for dg1_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dg1_1 protein demonstrated at least some similarity to sequences identified as M81878 (hyaluronidase [Clostridium perfringens]) and U28742 (similar to hyaluronoglucosaminidase (SPNAGH_CLOPE, P26831) [Caenorhabditis elegans]).
- 20 Hyaluronoglucosaminidase is a secreted protein found, for example, in bee venom. Based upon sequence similarity, dg1_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the dg1_1 protein sequence centered around amino acid 150 of SEQ ID NO:18.

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Clone "ep234_1"

- A polynucleotide of the present invention has been identified as clone "ep234_1". ep234_1 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was
- 30 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ep234_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ep234_1 protein").

The nucleotide sequence of ep234_1 as presently determined is reported in SEQ ID NO:19. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ep234_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20. Amino acids 59 to 71 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 72, or are a transmembrane domain.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ep234_1 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for ep234_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ep234_1 demonstrated at least some similarity with sequences identified as AA044714 (zf54d09.r1 Soares retina N2b4HR Homo sapiens cDNA clone 380753 5'), AA454840 (zx79d09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 809969 3'), AA470137 (zu11e01.s1 Soares testis NHT Homo sapiens cDNA clone 731544 3'), H24852 (yl42c11.r1 Homo sapiens cDNA clone 160916 5'), N64648 (yz87b06.s1 Homo sapiens cDNA clone 290003 3'), R45788 (Ha662-f Homo sapiens cDNA clone a662-f), T70546 (yd15b07.s1 Homo sapiens cDNA clone 108277 3'), W73481 (zd54e01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344472 3'), and W73553 (zd54e01.r1 Soares fetal heart). Based upon sequence similarity, ep234_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts at least two potential transmembrane domains within the ep234_1 protein sequence of SEQ ID NO:20.

Deposit of Clones

Clones ax318_3, bg140_1, bg465_2, bk291_3, bp537_4, cs431_2, cw976_1, cw1233_3, dg1_1, and ep234_1 were deposited on March 11, 1997 with the American Type Culture Collection as an original deposit under the Budapest Treaty and were given the accession number ATCC 98353, from which each clone comprising a particular polynucleotide is obtainable. All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b).

Each clone has been transfected into separate bacterial cells (*E. coli*) in this composite deposit. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the

appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Fig. 1. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of the oligonucleotide probe that was used to isolate each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

20

<u>Clone</u>	<u>Probe Sequence</u>
ax318_3	SEQ ID NO:21
bg140_1	SEQ ID NO:22
bg465_2	SEQ ID NO:23, SEQ ID NO:32
25 bk291_3	SEQ ID NO:24
bp537_4	SEQ ID NO:25
cs431_2	SEQ ID NO:26
cw976_1	SEQ ID NO:27
cw1233_3	SEQ ID NO:28
30 dg1_1	SEQ ID NO:29
ep234_1	SEQ ID NO:30

In the sequences listed above which include an N at position 2 that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a

nucleotide (such as , for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

~~200 The design of the oligonucleotide probe should preferably follow these~~

5 parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
- (b) It should be designed to have a T_m of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

- 10 The oligonucleotide should preferably be labeled with g-³²P ATP (specific activity 6000 Ci/mmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated
- 15 by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmole.

- The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 µl of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 µg/ml. The culture should preferably be
- 20 grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 µg/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other
- 25 known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

- The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with
- 30 NaOH) containing 0.5% SDS, 100 µg/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. ~~The filter is then preferably washed in~~ 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed

by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also

5 be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, *Bio/Technology* 10, 773-778 (1992) and in R.S. McDowell, *et al.*, *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a

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The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

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The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can

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be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that
5 has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense
10 polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed
15 herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein).
20 In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of
25 transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396;
30 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of

assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologs are those isolated from mammalian species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

	Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [†]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
10	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	<50	T _B *; 1xSSC	T _B *; 1xSSC
	C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	<50	T _D *; 1xSSC	T _D *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
15	F	RNA:RNA	<50	T _F *; 1xSSC	T _F *; 1xSSC
	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	<50	T _H *; 4xSSC	T _H *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	<50	T _J *; 4xSSC	T _J *; 4xSSC
20	K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	<50	T _L *; 2xSSC	T _L *; 2xSSC
	M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	<50	T _N *; 6xSSC	T _N *; 6xSSC
	O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
25	P	DNA:RNA	<50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	<50	T _R *; 4xSSC	T _R *; 4xSSC

[†] The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed

to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

- 5 *: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

- 10 $T_h - T_m$: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, $T_m(^{\circ}\text{C}) = 2(\# \text{ of A} + \text{T bases}) + 4(\# \text{ of G} + \text{C bases})$. For hybrids between 18 and 49 base pairs in length, $T_m(^{\circ}\text{C}) = 81.5 + 16.6(\log_{10}[\text{Na}^+]) + 0.41(\% \text{G} + \text{C}) - (600/\text{N})$, where N is the number of bases in the hybrid, and $[\text{Na}^+]$ is the concentration of sodium ions in the hybridization buffer ($[\text{Na}^+]$ for 1xSSC = 0.165 M).

- 15 Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

- 20 Preferably, each such hybridizing polynucleotide has a length that is at least 25%(more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

- 30 The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205

cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

~~2002~~ Alternatively, it may be possible to produce the protein in lower eukaryotes such
5 as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or
10 bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide
15 of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment
20 Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting
25 expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA
30 Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as

those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and ~~in vitro~~, respectively. The protein can also be tagged with an epitope and

5 subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or
10 all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic
15 animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are
20 known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic
25 compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications
30 of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art

(see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening

5 or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

10 The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies

15 or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express

20 recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare

25 with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for

30 examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that

described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

5 The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

20 Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

25 Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in*

- Immunology*, J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*, J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991;
- 5 Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*, J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

- Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in:
- 10 Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al.,
- 15 Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

- 20 A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well
- 25 as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses,
- 30 herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

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Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barré syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis,

5 myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present  
10 invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T  
15 cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to  
20 the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing  
25 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys  
30 the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the

molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to

5 anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

10 The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as  
15 described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

20 Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.  
25 Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from  
30 the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and

murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), ~~as a means of up-regulating immune responses~~, may also be useful in therapy.

- 5 Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B
- 10 lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary

costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro*



antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

- Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation,
- 5 those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.
  - 10 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995;
  - 15 Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research* 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993;
- 25 Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

- Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* 84:111-117, 1994; Fine et al., *Cellular Immunology* 155:111-122, 1994; Galy et al., *Blood* 85:2770-2778, 1995; Toki et al., *Proc. Nat. Acad Sci. USA* 88:7548-7551, 1991.

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#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell

lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and

Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

#### Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in

circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-

$\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion

- include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

- A protein of the invention may also exhibit hemostatic or thrombolytic activity.
- 10 As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting
- 15 therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

- Assay for hemostatic and thrombolytic activity include, without limitation, those
- 20 described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### Receptor/Ligand Activity

- 25 A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation,
- 30 cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without

limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 5 Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 10 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

#### Anti-Inflammatory Activity

- 15 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or 20 suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin 25 lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

#### Cadherin/Tumor Invasion Suppressor Activity

30 Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human



diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved  
5 extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin so that instead of recognizing only  
10 itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and the cancer metastasizes. Transfection of cancer cell lines with  
15 polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion  
20 suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the inappropriately expressed cadherins, restoring normal cell adhesive properties and  
30 reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from

forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

- 5 Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present  
 10 invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

- Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995;  
 15 Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

#### Tumor Inhibition Activity

- In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities.  
 20 A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating  
 25 or inhibiting factors, agents or cell types which promote tumor growth.

#### Other Activities

- A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious  
 30 agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or cardiac cycles or rhythms;

effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

#### 15 ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects.

of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical

5 compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B  
10 lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be  
15 supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

20 The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation,  
25 monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

30 As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active

ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein

of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1mg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such

antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in

5 R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions

10 associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage,

15 tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or

20 tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the

25 composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

30 The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and

polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other

5 ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

10 Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

15 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropylmethylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic  
20 acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells  
25 are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor  
30 (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.



The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

(1) GENERAL INFORMATION:

McCoy, John M.  
LaVallie, Edward R.  
Racie, Lisa A.  
Merberg, David  
Treacy, Maurice  
Spaulding, Vikki  
Agostino, Michael

(ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
ENCODING THEM

(iii) NUMBER OF SEQUENCES: 32

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.  
(B) STREET: 87 CambridgePark Drive  
(C) CITY: Cambridge  
(D) STATE: MA  
(E) COUNTRY: U.S.A.  
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sprunger, Suzanne A.  
(B) REGISTRATION NUMBER: 41,323

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 498-8284  
(B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1328 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

|    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |    |    |    |    |    |    |    |    |    |     |
|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|----|----|----|----|----|----|----|----|----|-----|
| 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |    |    |    |    |    |    |    |    |    |     |
| 1  | 2  | 3  | 4  | 5  | 6  | 7  | 8  | 9  | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90  | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |

(ii) MOLECULE TYPE: cDNA

|||||  
 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

CGTTAACAAG TGGAATGGAA CTCAAAGACA ATATTCTTGT CTCTGGGAAT GCAGATTCTA    60
CAGTTAAAAT CTGGGATATC AAAACAGGAC AGTGTTTACA AACATTGCAA GGTCCCAACA    120
AGCATCAGAG TGCTGTGACC TGTTTACAGT TCAACAAGAA CTTTGTAAAT ACCAGCTCAG    180
ATGATGGAAC TGTAATACTA TGGGACTTGA AAACGGGTGA ATTTATTCTGA AACCTAGTCA    240
CATTGGAGAG TGGGGGGAGT GGGGGAGTTG TGTGGCGGAT CACAGCCTCA AACACAAAGC    300
TGGTGTGTGC AGTTGGGAGT CGGAATGGGA CTGAAGAAAC CAAGCTGCTG GTGCTGGACT    360
TTGATGTGGA CATGAAGTGA AGAGCAGAAA AGATGAATTT GTCCAATTGT GTAGACGATA    420
TACTCCCTGC CCTCCCCCT GCAAAAAGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA    480
AAAAAAAAAA AAAAAAGCGC AAGCTCCAGG TTTCACCACA ATGCCCATCC CTGCCTCCCC    540
ACTCCACCCA CCTCTGCCTT CCTTACTGCT GTATCTGCTG CTTGAACTGG CAGGAGTCAC    600
ACATGTGTTC CATGTGCAAC AAACGGAGAT GTCACAGACT GTATCAACTG GGGAGTCAAT    660
CATCTTGAGT TGCAGCGTAC CCGATACCTT ACCAAATGGA CCTGTCTTGT GGTTC AAGGG    720
AACAGGGCCA AACCGGAAAT TAATCTACAA TTTCAAACAA GGTAAC TTTC CCAGAGTAAA    780
AGAGATTGGA GACACCACCA AGCCTGGCAA CACAGACTTT TCCACCCGCA TCCGTGAAAT    840
CTCTCTTGCT GATGCTGGCA CCTATTACTG CGTGAAGTTC ATAAAAGGAA GAGCTATCAA    900
GGAGTACCAA TCAGGTCGGG GCACTCAGGT GTTTGTTACT GAGCAGAATC CAAGACCTCC    960
CAAGAACAGA CCTGCAGGCA GAGCAGGCTC CAGGGCCCAC CATGATGCCC ATACCTGCCT    1020
CTCGGCCCTG CCTGAGAGAA ACAGCACAAA CTATTTCGTC CAACCCTGCT GCTGCCTCCG    1080
GCTGCTGGGA CTCACAGGCT TGCTGTCAAA ATAATCCAAA CAGGGAAGGA ACGTACAAGT    1140
AAATAACAAA AGCCCCCATA CTCTTCTGAC TCCCTGGAGA CAGCTACTTT TTAGGAGTTT    1200
CATTTGCCTT CTTCAAGAGA GCTTTCTTCC ACTGACATAA AATGCCAGCT TGATCGTACA    1260
ATAAATCTGT CTATTACCT GGGTCCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA    1320
AAAAAAAAA                                     1328
  
```

(2) INFORMATION FOR SEQ ID NO:2:

|||||

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met  Pro  Ile  Pro  Ala  Ser  Pro  Leu  His  Pro  Pro  Leu  Pro  Ser  Leu  Leu
1              5              10              15

Leu  Tyr  Leu  Leu  Leu  Glu  Leu  Ala  Gly  Val  Thr  His  Val  Phe  His  Val
                20              25              30

Gln  Gln  Thr  Glu  Met  Ser  Gln  Thr  Val  Ser  Thr  Gly  Glu  Ser  Ile  Ile
                35              40              45

Leu  Ser  Cys  Ser  Val  Pro  Asp  Thr  Leu  Pro  Asn  Gly  Pro  Val  Leu  Trp
50              55              60

Phe  Lys  Gly  Thr  Gly  Pro  Asn  Arg  Lys  Leu  Ile  Tyr  Asn  Phe  Lys  Gln
65              70              75              80

Gly  Asn  Phe  Pro  Arg  Val  Lys  Glu  Ile  Gly  Asp  Thr  Thr  Lys  Pro  Gly
                85              90              95

Asn  Thr  Asp  Phe  Ser  Thr  Arg  Ile  Arg  Glu  Ile  Ser  Leu  Ala  Asp  Ala
                100             105             110

Gly  Thr  Tyr  Tyr  Cys  Val  Lys  Phe  Ile  Lys  Gly  Arg  Ala  Ile  Lys  Glu
                115             120             125

Tyr  Gln  Ser  Gly  Arg  Gly  Thr  Gln  Val  Phe  Val  Thr  Glu  Gln  Asn  Pro
130              135              140

Arg  Pro  Pro  Lys  Asn  Arg  Pro  Ala  Gly  Arg  Ala  Gly  Ser  Arg  Ala  His
145              150              155              160

His  Asp  Ala  His  Thr  Cys  Leu  Ser  Ala  Leu  Pro  Glu  Arg  Asn  Ser  Thr
                165              170              175

Asn  Tyr  Phe  Val  Gln  Pro  Cys  Cys  Cys  Leu  Arg  Leu  Leu  Gly  Leu  Thr
                180              185              190

Gly  Leu  Leu  Ser  Lys
                195

```

## (2) INFORMATION FOR SEQ ID NO:3:

=====

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2835 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GCTTGATAAG CCAGCTTCAG GAGTAAAGGA AGAATGGTAT GCCAGAATCA CTAAATTAAG | 60   |
| ATGGTGGATC AGCTTTTCTG CAAAAAATTT GCGGAAGCCT TGGGGAGCAC TGAAGCCAAG | 120  |
| GCTGTACCGT ACCAAAAATT TGAGGCACAC CCGAATGATC TGTACGTGGA AGGACTGCCA | 180  |
| GAAAACATTC CTTTCCGAAG TCCCTCATGG TATGGAATCC CAAGGCTGGA AAAAATCATT | 240  |
| CAAGTGGGCA ATCGAATTAA ATTTGTTATT AAAAGACCAG AACTTCTGAC TCACAGTACC | 300  |
| ACTGAAGTTA CTCAGCCAAG AACGAATACA CCAGTCAAAG AAGATTGGAA TGTCAGAATT | 360  |
| ACCAAGCTAC GGAAGCAAGT GGAAGAGATT TTTAATTGTA AATTGCTCA AGCTCTTGGA  | 420  |
| CTCACCGAGG CAGTAAAAGT ACCATATCCT GTGTTTGAAT CAAACCCGGA GTTCTTGTAT | 480  |
| GTGGAAGGCT TGCCAGAGGG GATTCCTTC CGAAGCCCTA CCTGGTTTGG AATTCCACGA  | 540  |
| CTTGAAAGGA TCGTCCACGG GAGTAATAAA ATCAAGTTCG TTGTTAAAAA ACCTGAACTA | 600  |
| GTTATTTCTT ACTTGCCCTC TGGGATGGCT AGTAAATAAA ACACTAAAGC TTTGCAGTCC | 660  |
| CCCAAAGAC CACGAAGTCC TGGGAGTAAT TCAAAGGTTT CTGAAATTGA GGTCACCGTG  | 720  |
| GAAGGCCYTA ATAACAACAA TCCTCAAACC TCAGCTGTTC GAACCCCGAC CCAGACTAAC | 780  |
| GGTTCTAACG TTCCCTTCAA GCCACGAGGG AGAGAGTTTT CCTTTGGCCT GGAATGCCAA | 840  |
| AATCACGGAC CTAAACAGA AAGTTGAAAA TCTCTTCAAT GAGAAATGTG GGGAAGCTCT  | 900  |
| TGGCCTTAAA CAAGCTGTGA AGGTGCCGTT CGCGTTATTT GAGTCTTTCC CGGAAGACTT | 960  |
| TTATGTGGAA GGCTTACCTG AGGGTGTGCC ATTCCGAAGA CCATCGACTT TTGGCATTCC | 1020 |
| GAGGCTGGAG AAGATACTCA GAAACAAAGC CAAAATTAAG TTCATCATTA AAAAGCCCGA | 1080 |
| AATGTTTGAG ACGGCGATTA AGGAGAGCAC CTCCTCTAAG AGCCCTCCCA GAAAAATAAA | 1140 |
| TTCATCACCC AATGTTAATA CTACTGCATC AGGTGTTGAA GACCTTAACA TCATTCAAGT | 1200 |
| GACAATTCCA GATGATGATA ATGAAAGACT CTCGAAAGTT GAAAAAGCTA GACAGCTAAG | 1260 |
| AGAACAAGTG AATGACCTCT TTAGTCGGAA ATTTGGTGAA GCTATTGGTA TGGGTTTTC  | 1320 |

TGTGAAAGTT CCCTACAGGA AAATCACAAT TAACCCTGGC TGTGTGGTGG TTGATGGCAT 1380  
 GCCCCCGGGG GTGTCCTTCA AAGCCCCCAG CTACCTGGAA ATCAGCTCCA TGAGAAGGAT 1440  
 CTTAGACTCT GCCGAGTTTA TCAAATTCAC GGTCAATTAGA CCATTTCAG GACTTGTGAT 1500  
 TAATAACCAG CTGGTTGATC AGAGTGAGTC AAAAGGCCCC GTGATACAAG AATCAGCTGA 1560  
 ACCAAGCCAG TTGGAAGTTC CAGCCACAGA AGAAATAAAA GAGACTGATG GAAGCTCTCA 1620  
 GATCAAGCAA GAACCAGACC CCACGTGGTA GACCTCTTCC CTCCTAGGCT TAAAGTATCA 1680  
 GTGGTTGAGA AGAGCTTTTC GGACCTGTTA CTACCCCAAG CTGTGTAATA TACTTGTATA 1740  
 ACAGAAATAC CTTCTATACA AACCTTTTTT TCTACTTTTA GATAGAAATG TCTACTTTTT 1800  
 CAGCAGTTCT GTGAATTAAA GAGCAGAGTG ACTGTGGGTC TGAATGGCT GGTGTACTTG 1860  
 GGAATGTACT ATCAGGATTT TACAGCAATG CTGGGAAATG ACAGGGAAAA TGACAGGAAT 1920  
 GAATCTCACC AGATTTTTTA TGTACTCAGC AGAGCCTTGA GTTACGGTGT TTATTTTCCA 1980  
 ATCAAGTGAA GATATCTCCT ACTTCTCCTA CTGGAACATC TCAGCTTCTG CAGTGAAGAA 2040  
 AAATTCCTGT GATAGTTCAG TTCTTTAGTT TTTCTATTTG AAAAAAAAAA ATCATTTAAA 2100  
 TGATCCTTTG TTCACGGCTC TCCTTAATGA CTGAGTGAAC AGTTCCTATC TGTATATTTG 2160  
 ACTAAACCTT TTCCTAAGCT ATCTCTCATG GTTCCTATGT TTTTATATCA TAATTAAAAG 2220  
 CAAAACCATT TGGATCACCT AACAGTCAGA GGTCAGTATC TCAGCGTGTG AATTATAGAG 2280  
 GAAATACAGA GAGAACCTCT TCCACTTTTA CTTTTCGTCC AAATAAAATG CATGGTGTAC 2340  
 CAGAAGTTGA AGATCGGGTT GAGGATTGGG GCTAGCTCGA TGACACTAAG GCCCCAACAT 2400  
 CGCGGGACCT GCTGTGGCGC GGATTCTTAG GAACGCTGTT CTAGCCGGCC CCCTCTCCAG 2460  
 GGGTCGCCGT GGCCGGCATT ATTTCTAGT TCTTCTTGTA ACCCTGAGGT GCCAGCGCGG 2520  
 GGAGTGAGGA GGGGTCAGGG GGCTAAGGAT GCAACCTCTG ACGTTCTGCG CCTTCCTAGG 2580  
 AGAGTCTTAC ATGTGTTGAG ATTTACACAAG CAATGCGAGT TGTAATAATC CAGCTCTACA 2640  
 AGAAGCTAGG CTCTGTGACG GCATAGTTTT CAGTAGCTTT ATCACAATAT TCACAATGGA 2700  
 GAATTATATG ACATGGTAGC AGAAATAGGC CCTTTTATGT GTTGCTTCTA TTTTACCTCA 2760  
 AATTGTAGAT ATAGGGTAAT CAATAAAATC CATCCATGCC TTTCAAAAAA AAAAAAAAAA 2820  
 AAAAAAAAAA AAAAA 2835

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

100 1000 2000 3000 4000 5000 6000 7000 8000 9000 10000

(A) LENGTH: 268 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Val Asp Gln Leu Phe Cys Lys Lys Phe Ala Glu Ala Leu Gly Ser
1           5           10          15

Thr Glu Ala Lys Ala Val Pro Tyr Gln Lys Phe Glu Ala His Pro Asn
20          25          30

Asp Leu Tyr Val Glu Gly Leu Pro Glu Asn Ile Pro Phe Arg Ser Pro
35          40          45

Ser Trp Tyr Gly Ile Pro Arg Leu Glu Lys Ile Ile Gln Val Gly Asn
50          55          60

Arg Ile Lys Phe Val Ile Lys Arg Pro Glu Leu Leu Thr His Ser Thr
65          70          75          80

Thr Glu Val Thr Gln Pro Arg Thr Asn Thr Pro Val Lys Glu Asp Trp
85          90          95

Asn Val Arg Ile Thr Lys Leu Arg Lys Gln Val Glu Glu Ile Phe Asn
100         105         110

Leu Lys Phe Ala Gln Ala Leu Gly Leu Thr Glu Ala Val Lys Val Pro
115         120         125

Tyr Pro Val Phe Glu Ser Asn Pro Glu Phe Leu Tyr Val Glu Gly Leu
130         135         140

Pro Glu Gly Ile Pro Phe Arg Ser Pro Thr Trp Phe Gly Ile Pro Arg
145         150         155         160

Leu Glu Arg Ile Val His Gly Ser Asn Lys Ile Lys Phe Val Val Lys
165         170         175

Lys Pro Glu Leu Val Ile Ser Tyr Leu Pro Pro Gly Met Ala Ser Lys
180         185         190

Ile Asn Thr Lys Ala Leu Gln Ser Pro Lys Arg Pro Arg Ser Pro Gly
195         200         205

Ser Asn Ser Lys Val Pro Glu Ile Glu Val Thr Val Glu Gly Xaa Asn
210         215         220

Asn Asn Asn Pro Gln Thr Ser Ala Val Arg Thr Pro Thr Gln Thr Asn

```

225                      230                      235                      240  
 Gly Ser Asn Val Pro Phe Lys Pro Arg Gly Arg Glu Phe Ser Phe Gly  
                          245                      250                      255  
 Leu Glu Cys Gln Asn His Gly Pro Lys Thr Glu Ser  
                          260                      265

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TAGGCCATGA AGGCCGCGCT TTTCGTCGAC TCTTACCGGT TGGCTGGGCC AGCTGCGCCG 60  
 CGGCTCACAG CTGACCATGG GGGACCCAG CAAGCAGGAC ATCTTGACCA TCTTCAAGCG 120  
 CCTCCGCTCG GTGCCCATA ACAAGGTGTG TTTTGATTGT GGTGCCAAAA ATCCCAGCTG 180  
 GGCAAGCATA ACCTATGGAG TGTTCCTTTG CATTGATTGC TCAGGGTCCC ACCGGTCACT 240  
 TGGTGTTCAC TTGAGTTTTA TTCGATCTAC AGAGTTGGAT TCCAAGTGGT CATGGTTTCA 300  
 GTTGCGATGC ATGCAAGTCG GAGGAAACGC TAGTGCATCT TCCTTTTTTC ATCAACATGG 360  
 GTGTTCCACC AATGACACCA ATGCCAAGTA CAACAGTCGT GCTGCTCAGC TCTATAGGGA 420  
 GAAAATCAAA TCGCTCGCCT CTCAAGCAAC ACGGAAGCAT GGCATGATC TGTGGCTTGA 480  
 TAGTTGTGTG GTTCCACCTT TGTCCCCTCC ACCAAAGGAG GAAGATTTTT TTGCCTCTCA 540  
 CGTTTCTCCT GAGGTGAGTG ACACAGCGTG GGCATCAGCA ATAGCAGAAC CATCTTCTTT 600  
 AACATCAAGG CCTGTGGAAG CCACTTTGGA AAATAATGAA GGTGGACAAG AGCAAGGACC 660  
 AAGTGTGGAA GGTCTTAATG TACCAACAAA GGCTACTTTA GAGGTATCCT CTATCATAAA 720  
 AAAGAAACCA AATCAAGCTA AAAAAGGCCT TGGGGCCAAA AAAGGAAGTT TGGGAGCTCA 780  
 GAAACTGGCA AACACATGCT TTAATGAAAT TGAAAAACAA GCTCAAGCTG CGGATAAAAT 840  
 GAAGGAGCAG AAAGACCTGG CCAAGGTGGT ATCTAAAGAA GAATCAATTG TTTCATCATT 900  
 ACGATTAGCC TATAAGGATC TTGAAATTCA AATGAAGAAA GACCAATAGA TGAACATTAG 960



TGGCAAAAAA AATGTTGACT CAGACAGACT CGGCATGGGA TTTGGAAATT GCAGAAGTGT 1020  
 TATTTACAT. TCAGTGACTT CAGATATGCA GACCATAGAG CAGGAATCAC CCATTATGGC 1080  
~~AAAAGCAAGA AAAAGTATA ATGATGACAG TGACGATTCA TATTTTACTT CCAGCTCAAG~~ 1140  
 TTACTTTGAC GAGCCAGTGG AGTTAAGGAG CAGTTCTTTC TCTAGCTGGG ATGACAGTTC 1200  
 AGATTCCCTAT TGGAAAAAAG AGACCAGCAA AGATACTGAA ACAGTTCTGA AAACCACAGG 1260  
 CTATTACAGAC AGACCTACTG CTCGCCGCAA GCCAGATTAT GAGCCAGTTG AAAATACAGA 1320  
 TGAGGCCCCAG AAGAAGTTTG GCAATGTCAA GGCCATTTC A TCAGATATGT ATTTTGGAAAG 1380  
 ACAATCCCAG GCTGATTATG AGACCAGGGC CCGCCTAGAG AGGCTGTCGG CAAGTTCCTC 1440  
 CATAAGCTCG GCTGATCTGT TCGAGGAGCC GAGGAAGCAG CCAGCAGGGA ACTACAGCCT 1500  
 GTCCAGTGTG CTGCCCAACG CCCCCGACAT GGCGCAGTTC AAGCAGGGAG TGAGATCGGT 1560  
 TGCTGGAAAA CTCTCCGTCT TTGCTAATGG AGTCGTGACT TCAATTCAGG ATCGCTACGG 1620  
 TTCTTAATAC TGAAGTCATG ATGTGTATTT CCTGGAGAAA TTCCTCTTTA AATGAACAAG 1680  
 TAACCACATC TCAGGCGGCA GTGAAGTCCA GATAGTTTTG CAGATTGTTT TGCTACTTTT 1740  
 TCATATGGTA TATGTTTCTG ATTTTAAATA TTTCTTTTGA GAAATTCTGA GTTCTGATGT 1800  
 AGGAGCTTTC CTGTGATTTT TGTTCACGT TCCTTCCTGT CACACCCTCC TTTGGCGTCT 1860  
 CTGTGTATAT CCTTGCTTTA TTTTCTTGGA ACCTTGATT TCAACACTGA GGGCCTGGAG 1920  
 ACCTCGGCTC CTCCTGCTCC TGAACCAGGA GGCTTCATGT GGGGGAGGAG GAGAGGTCTC 1980  
 CATGTGACAC ATGGGCTCAG GGCTGCCAGA ATCAGCGGAT GCTGGATGGG CCTGCAGAAA 2040  
 CAACACTCAC CACACACACT TCCTTCAAAA GACCAAAAGT GACTGGTGTC TCGTGTGACA 2100  
 GATTGCTTCA TTTATGTTTC TACATAGTAA GGTGACTGCC AAATAATATT TGAAGTCATC 2160  
 TGTCTCTTTG TAAATTATTT TATATGACCT ATAAATTTAA AAATGTTTTT CAGTGAGTGC 2220  
 TTTTAACAAA CTTAAGCTTC TGCCCTGCCA AGGGAATTAA TGTTATCTTG TGAAAGGTGT 2280  
 TGCTGTTTGA ATTGATGAGA AATGGAAGAT GAGAACTCCC TAAGAGTTCT CATAATAAAT 2340  
 CATCTCATCA CAAATCAATA CGGTATACAG AGTTAAAGTG GAATGAGGTA AGAAGATACA 2400  
 GCTACAGAAA ATAGTTGCGT GTATGGGAGA ACAGTCATTG TAATTGGGTA GTTTTGTTAA 2460  
 TAAATATTTT TAAATCTTGC TTTTCAGAAA TTACCGAATG TGTATAAACA AATAAAGAAA 2520  
 AATAATTTAG CTGTGTTTTA GACAGCATTA GAATATTTG ~~TTGAGCAGAG TAAATATAT~~ 2580  
 TTGAAATTTG ATAAGCCAAA AATGTGGTTT TGAATGAATA TTTGTGAAT CTTTCTTAAA 2640

AGCTCAAATT TGTAGACTTC TAAATAGAAT AAACACTTGC AGCAGATGGA AAAAAAAAAA 2700

AAAAA 2705

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Asp | Pro | Ser | Lys | Gln | Asp | Ile | Leu | Thr | Ile | Phe | Lys | Arg | Leu | 1   | 5   | 10  | 15  |
| Arg | Ser | Val | Pro | Thr | Asn | Lys | Val | Cys | Phe | Asp | Cys | Gly | Ala | Lys | Asn | 20  | 25  | 30  |     |
| Pro | Ser | Trp | Ala | Ser | Ile | Thr | Tyr | Gly | Val | Phe | Leu | Cys | Ile | Asp | Cys | 35  | 40  | 45  |     |
| Ser | Gly | Ser | His | Arg | Ser | Leu | Gly | Val | His | Leu | Ser | Phe | Ile | Arg | Ser | 50  | 55  | 60  |     |
| Thr | Glu | Leu | Asp | Ser | Asn | Trp | Ser | Trp | Phe | Gln | Leu | Arg | Cys | Met | Gln | 65  | 70  | 75  | 80  |
| Val | Gly | Gly | Asn | Ala | Ser | Ala | Ser | Ser | Phe | Phe | His | Gln | His | Gly | Cys | 85  | 90  | 95  |     |
| Ser | Thr | Asn | Asp | Thr | Asn | Ala | Lys | Tyr | Asn | Ser | Arg | Ala | Ala | Gln | Leu | 100 | 105 | 110 |     |
| Tyr | Arg | Glu | Lys | Ile | Lys | Ser | Leu | Ala | Ser | Gln | Ala | Thr | Arg | Lys | His | 115 | 120 | 125 |     |
| Gly | Thr | Asp | Leu | Trp | Leu | Asp | Ser | Cys | Val | Val | Pro | Pro | Leu | Ser | Pro | 130 | 135 | 140 |     |
| Pro | Pro | Lys | Glu | Glu | Asp | Phe | Phe | Ala | Ser | His | Val | Ser | Pro | Glu | Val | 145 | 150 | 155 | 160 |
| Ser | Asp | Thr | Ala | Trp | Ala | Ser | Ala | Ile | Ala | Glu | Pro | Ser | Ser | Leu | Thr | 165 | 170 | 175 |     |
| Ser | Arg | Pro | Val | Glu | Thr | Thr | Leu | Glu | Asn | Asn | Glu | Gly | Gly | Gln | Glu | 180 | 185 | 190 |     |

Gln Gly Pro Ser Val Glu Gly Leu Asn Val Pro Thr Lys Ala Thr Leu  
 195 200 205  
 Glu Val Ser Ser Ile Ile Lys Lys Lys Pro Asn Gln Ala Lys Lys Gly  
 210 215 220  
 Leu Gly Ala Lys Lys Gly Ser Leu Gly Ala Gln Lys Leu Ala Asn Thr  
 225 230 235 240  
 Cys Phe Asn Glu Ile Glu Lys Gln Ala Gln Ala Ala Asp Lys Met Lys  
 245 250 255  
 Glu Gln Lys Asp Leu Ala Lys Val Val Ser Lys Glu Glu Ser Ile Val  
 260 265 270  
 Ser Ser Leu Arg Leu Ala Tyr Lys Asp Leu Glu Ile Gln Met Lys Lys  
 275 280 285  
 Asp Glu Lys Met Asn Ile Ser Gly Lys Lys Asn Val Asp Ser Asp Arg  
 290 295 300  
 Leu Gly Met Gly Phe Gly Asn Cys Arg Ser Val Ile Ser His Ser Val  
 305 310 315 320  
 Thr Ser Asp Met Gln Thr Ile Glu Gln Glu Ser Pro Ile Met Ala Lys  
 325 330 335  
 Pro Arg Lys Lys Tyr Asn Asp Asp Ser Asp Asp Ser Tyr Phe Thr Ser  
 340 345 350  
 Ser Ser Ser Tyr Phe Asp Glu Pro Val Glu Leu Arg Ser Ser Ser Phe  
 355 360 365  
 Ser Ser Trp Asp Asp Ser Ser Asp Ser Tyr Trp Lys Lys Glu Thr Ser  
 370 375 380  
 Lys Asp Thr Glu Thr Val Leu Lys Thr Thr Gly Tyr Ser Asp Arg Pro  
 385 390 395 400  
 Thr Ala Arg Arg Lys Pro Asp Tyr Glu Pro Val Glu Asn Thr Asp Glu  
 405 410 415  
 Ala Gln Lys Lys Phe Gly Asn Val Lys Ala Ile Ser Ser Asp Met Tyr  
 420 425 430  
 Phe Gly Arg Gln Ser Gln Ala Asp Tyr Glu Thr Arg Ala Arg Leu Glu  
 435 440 445  
 Arg Leu Ser Ala Ser Ser Ser Ile Ser Ser Ala Asp Leu Phe Glu Glu  
 450 455 460  
 Pro Arg Lys Gln Pro Ala Gly Asn Tyr Ser Leu Ser Ser Val Leu Pro  
 465 470 475 480  
 Asn Ala Pro Asp Met Ala Gln Phe Lys Gln Gly Val Arg Ser Val Ala

Arg Tyr Gly Ser  
515

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCATCGGTTT TCCTGTCCTG GTGGCGCTGG CCAAGGGAGAG AGTGACAGAG ATGTTCAGAT

```

ATGAGGAGTC AAATCCTAAG GATCCAGCGG CAGTGACAGA ATCCAAAGAG GGAACAGAGG 1020
CATCAGCATC GAAGGGGCTG GAGAAGAAAG AGAAATGATG CAGCTGGTGC CCGAGCCTCT 1080
CAGGGCCAGA CCAGACAGAT GGGGGCTGGG GCCACACAGG CGTGCACCGG TAGAGGGCAC 1140
AGGAGGCCAA GGGCAGCTCC AGGACAGGGC AGGGGGCAGC AGGATACCTC CAGCCAGGCC 1200
TCTGTGGCCT CTGTTTCCTT CTCCCTTTCT TGGCCCTCCT CTGCTCCTCC CCACACCCTG 1260
CAGGCAAAAG AAACCCCCAG CTTCCCCCT CCCCGGGAGC CAGGTGGGAA AAGTGGGTGT 1320
GATTTTTAGA TTTTGTATTG TGGACTGATT TTGCCTCACA TTAAAACTC ATCCCATGGC 1380
CAGGGCGGGC CACTGTAAAA AAAAAAAAAA AAAA 1414

```

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Ala Leu Leu Pro Ile Phe Phe Gly Ala Leu Arg Ser Val Arg Cys
1           5           10           15

Ala Arg Gly Lys Asn Ala Ser Asp Met Pro Glu Thr Ile Thr Ser Arg
20           25           30

Asp Ala Ala Arg Phe Pro Ile Ile Ala Ser Cys Thr Leu Leu Gly Leu
35           40           45

Tyr Leu Phe Phe Lys Ile Phe Ser Gln Glu Tyr Ile Asn Leu Leu Leu
50           55           60

Ser Met Tyr Phe Phe Val Leu Gly Ile Leu Ala Leu Ser His Thr Ile
65           70           75           80

Ser Pro Phe Met Asn Lys Phe Phe Pro Ala Ser Phe Pro Asn Arg Gln
85           90           95

Tyr Gln Leu Leu Phe Thr Gln Gly Ser Gly Glu Asn Lys Glu Glu Ile
100          105          110

Ile Asn Tyr Glu Phe Asp Thr Lys Asp Leu Val Cys Leu Gly Leu Ser
115          120

```

```

Ser Ile Val Gly Val Trp Tyr Leu Leu Arg Lys His Trp Ile Ala Asn
130                      135                      140

Asn Leu Phe Gly Leu Ala Phe Ser Leu Asn Gly Val Glu Leu Leu His
145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160
Leu Asn Asn Val Ser Thr Gly Cys Ile Leu Leu Gly Gly Leu Phe Ile
165                      170                      175

Tyr Asp Val Phe Trp Val Phe Gly Thr Asn Val Met Val Thr Val Ala
180                      185                      190

Lys Ser Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu
195                      200                      205

Glu Lys Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp
210                      215                      220

Val Val Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg Phe Asp Ile
225                      230                      235                      240

Ser Leu Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala
245                      250                      255

Tyr Ile Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys
260                      265                      270

His Ala Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe
275                      280                      285

Pro Val Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser
290                      295                      300

Tyr Glu Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys
305                      310                      315                      320

Glu Gly Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys
325                      330                      335

```

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: 1583 bp cDNA

78

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

~~~~~

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Leu Leu Tyr Ile Ala Asp Asn Leu Ala Cys Phe Pro Tyr Gln Thr
1           5           10           15

Gln Glu Glu Pro Leu Phe Ile Met His His Ile Asp Ile Thr Leu Ser
          20           25           30

Val Ser Gly Ser Asn Leu Leu Gln Ser Phe Lys Glu Ser Met Val Lys
          35           40           45

Asp Lys Arg Lys Glu Arg Lys Ser Ser Pro Ser Lys Glu Asn Glu Ser
          50           55           60

Ser Asp Ser Glu Glu Glu Val Ser Arg Pro Arg Lys Ser Arg Lys Arg
          65           70           75           80

Val Asp Ser Asp Ser Asp Ser Asp Ser Glu Asp Asp Ile Asn Ser Val
          85           90           95

Met Lys Cys Leu Pro Glu Asn Ser Ala Pro Leu Ile Glu Phe Ala Asn
          100          105          110

Val Ser Gln Gly Ile Leu Leu Leu Leu Met Leu Lys Gln His Leu Lys
          115          120          125

Asn Leu Cys Gly Phe Ser Asp Ser Lys Ile Gln Lys Tyr Ser Pro Ser
          130          135          140

Glu Ser Ala Lys Val Tyr Asp Lys Ala Ile Asn Arg Lys Thr Gly Val
          145          150          155          160

His Phe His Pro Lys Gln Thr Leu Asp Phe Leu Arg Ser Asp Met Ala
          165          170          175

Asn Ser Lys Ile Thr Glu Glu Val Lys Arg Ser Ile Val Lys Gln Tyr
          180          185          190

Leu Asp Phe Lys Leu Leu Met Glu His Leu Asp Pro Asp Glu Glu Glu
          195          200          205

Glu Glu Gly Glu Val Ser Ala Ser Thr Asn Ala Arg Asn Lys Ala Ile
          210          215 ~~~~~

```



```

Thr Ser Leu Leu Gly Gly Gly Ser Pro Lys Asn Asn Thr Ala Ala Glu
225                               230                               235                               240

Thr Glu Asp Asp Glu Ser Asp Gly Glu Asp Arg Gly Gly Gly Thr Ser
245                               250                               255
Gly Ser Leu Arg Arg Ser Lys Arg Asn Ser Asp Ser Thr Glu Leu Ala
260                               265                               270

Ala Gln Met Asn Glu Ser Val Asp Val Met Asp Val Ile Ala Ile Cys
275                               280                               285

Cys Pro Lys Tyr Lys Asp Arg Pro Gln Ile Ala Arg Val Val Gln Lys
290                               295                               300

Thr Ser Ser Gly Phe Ser Val Gln Trp Met Ala Gly Ser Tyr Ser Gly
305                               310                               315                               320

Ser Trp Thr Glu Ala Lys Arg Arg Asp Gly Arg Lys Leu Val Pro Trp
325                               330                               335

Val Asp Thr Ile Lys Glu Ser Asp Ile Ile Tyr Lys Lys Ile Ala Leu
340                               345                               350

Thr Ser Ala Asn Lys Leu Thr Asn Lys Val Val Gln Thr Leu Arg Ser
355                               360                               365

Leu Tyr Ala Ala Lys Asp Gly Thr Ser Ser
370                               375

```

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

TCCCGTCGCG CTCAGCATCC TCAATCATCC GCAGGCTGAT GCGGTCCTTC ACGCTCCCGC      60
CCGCGTTGAA GAACTCACAC TTGGCCAAGA GCTCACACTT CAGGCCGAAC TTCTTCCCAA      120
TCTTGTGAT TCTGACCATA GGGGTGTCCC CGATTTTCTT CAGAATATCT GGCAAGATTT      180
TTGGAGATTT TGCCGGGGCA GTGTGGTGAT GTGGGGACTC GGAGGCAGGC CGGCCAGCT      240
GCCAGGTGCA CCTGCTCGGA GCATCGGGCC GGATCCAGAG GGGGTCCTTG GCTTCCTTAT TTTTCTT

```

CCTCTGGGGA CCCCTTCTCC AGGCTCCCCCT TCGCCGAGTG TGGCCCTGAG CGGTGGGGGC 360
 AGCCTGTGGG CCCCACTTCT GCCTGGGGGG TCTCAGAAGG CATGCTGGGA CCGGACAGAT 420
 GGTGCTGACA GTTCAGCACC GCTCAAATCT TGTAAGGAGA CGTGACAACA GAATCTGTCA 480
 TGGGATCCTG GAATAGAAAA GGGCAGTGAG GAGAAACTC TGCAAATCTG ACTCAAGCGC 540
 GGACTTTGGT TAGGCCTCTT TGGACAGTAC TTTGAGAATT ATGGATCTCC GGATATTAGT 600
 AGCAAGGAAG TTTGTAGGAG CAGCAAATTA TCGGGAGAAG ATTCATAGTA CTTTGACTCC 660
 ATGTGGGACT TTTCTGTTTG CTGGAAGTGA GGATGGTATA GTGTATGTTT GGAACCCAGA 720
 AACAGGAGAA CAAGTAGCCA TGTATTCTGA CTTGCCATTC AAGTCACCCA TTCGAGACAT 780
 TTCTTATCAT CCATTTGAAA ATATGGTTGC ATTCTGTGCA TTTGGGCAAA ATGAGCCAAT 840
 TCTTCTGTAT ATTTACGATT TCCATGTTGC CCAGCAGGAG GCTGAAATGT TCAAACGCTA 900
 CAATGGAACA TTTCCATTAC CTGGAATACA CCAAAGTCAA GATGCCCTAT GTACCTGTCC 960
 AAAACTACCC CATCAAGGCT CTTTTCAGAT TGATGAATTT GTCCACACTG AAAGTTCTTC 1020
 AACGAAGATG CAGCTAGTAA AACAGAGGCT TGAAACTGTC ACAGAGGTGA TACGTTCTCTG 1080
 TGCTGCAAAA GTCAACAAAA ATCTCTCATT TACTTCACCA CCAGCAGTTT CCTCACAACA 1140
 GTCTAAGTTA AAGCAGTCAA ACATGCTGAC CGCTCAAGAG ATTCTACATC AGTTTGGTTT 1200
 CACTCAGACC GGGATTATCA GCATAGAAAG AAAGCCTTGT AACCATCAGG TAGATACAGC 1260
 ACCAACGGTA GTGGCTCTTT ATGACTACAC AGCGAATCGA TCAGATGAAC TAACCATCCA 1320
 TCGCGGAGAC ATTATCCGAG TGTTTTTCAA AGATAATGAA GACTGGTGGT ATGGCAGCAT 1380
 AGGAAAGGGA CAGGAAGGTT ATTTTCCAGC TAATCATGTG GCTAGTGAAA CACTGTATCA 1440
 AGAACTGCCT CCTGAGATAA AGGAGCGATC CCCTCCTTTA AGCCCTGAGG AAAAAACTAA 1500
 AATAGAAAAA TCTCCAGCTC CTCAAAGGT AAAATAAAAC AAAACAGCTC ACAGAGACAC 1560
 CTCCTTCTTC CCCCTGCTTC TGCCTCCATG AGTAACTACC TATATGACGT GCTGCTGCTG 1620
 AGACCAAGGA ATGAGTGAGT AAAGGTGTTT GGAAGTCAAA TATTGGTCCT AGTTAAGTAA 1680
 GTGTCCTTTT CAAGTAAGTG GTAAACTTTG TAATGTGGAC CCCCTTCTAA CTTAGGATTC 1740
 ATATAATTTG AACACAGGCT AAGCTGCCTC TGCATCATTA AAAAGGATTT GGGTATGCCA 1800
 GTGATAGGAA TACACAGTAG AAAAGATGGC AGGGACCATG TTTAACATAC CTAAGACAAA 1860
 CTTTCTGAGG ATATCACAGC ATCCATTTCA CATGAACAGA CTTAGCAGAA TTGGCAAGAC 1920
 CTGCACATGG CAACATATTA TTCATTTTTC AGGATAACAA AAAATAATTA AAAGTAACAT 1980

```

TGGCTTAACA CTGGTATATA GTTCAGTATG ACTTCTCTCC CCTCAACCTC TGGAAATAGGT    2040
TCAAATTGAT GAGAATTTCT GATTAGAGCC CTTAATGTTG AGTTTTTTGA AAAGTTTAT      2100
CAAGTTTCAT ATATAGCTAT ATTGATGGTA AGTTGCTGGT CTTGCCATGG GCAAAGAGAG    2160
AAAAATGATA YTGAGACCTT GTAAAGAATA GYTGGACATG GAGGCGCACA CCTGTAATCC      2220
CAGCAAYTCA GAAGGCTGAG GCGGGAGGAT TGCTTGAGCC CAGGAGTTCA AGGCTGCAGT      2280
GAGCTACGAT CATGCCACTG TACTCCAGCC TGAGCAACAA AGCATGACCC AATCTCTTAA      2340
AAAAAAAAAA AAA                                                              2353

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Met Asp Leu Arg Ile Leu Val Ala Arg Lys Phe Val Gly Ala Ala Asn
1           5           10           15
Tyr Arg Glu Lys Ile His Ser Thr Leu Thr Pro Cys Gly Thr Phe Leu
20           25           30
Phe Ala Gly Ser Glu Asp Gly Ile Val Tyr Val Trp Asn Pro Glu Thr
35           40           45
Gly Glu Gln Val Ala Met Tyr Ser Asp Leu Pro Phe Lys Ser Pro Ile
50           55           60
Arg Asp Ile Ser Tyr His Pro Phe Glu Asn Met Val Ala Phe Cys Ala
65           70           75           80
Phe Gly Gln Asn Glu Pro Ile Leu Leu Tyr Ile Tyr Asp Phe His Val
85           90           95
Ala Gln Gln Glu Ala Glu Met Phe Lys Arg Tyr Asn Gly Thr Phe Pro
100          105          110
Leu Pro Gly Ile His Gln Ser Gln Asp Ala Leu Cys Thr Cys Pro Lys
115          120          125
Leu Pro His Gln Gly Ser Phe Gln Ile Asp Gln Phe Val His Thr Glu
130          135          140

```

Ser Ser Ser Thr Lys Met Gln Leu Val Lys Gln Arg Leu Glu Thr Val
 145 150 155 160

Thr Glu Val Ile Arg Ser Cys Ala Ala Lys Val Asn Lys Asn Leu Ser
 165 170 175

Phe Thr Ser Pro Pro Ala Val Ser Ser Gln Gln Ser Lys Leu Lys Gln
 180 185 190

Ser Asn Met Leu Thr Ala Gln Glu Ile Leu His Gln Phe Gly Phe Thr
 195 200 205

Gln Thr Gly Ile Ile Ser Ile Glu Arg Lys Pro Cys Asn His Gln Val
 210 215 220

Asp Thr Ala Pro Thr Val Val Ala Leu Tyr Asp Tyr Thr Ala Asn Arg
 225 230 235 240

Ser Asp Glu Leu Thr Ile His Arg Gly Asp Ile Ile Arg Val Phe Phe
 245 250 255

Lys Asp Asn Glu Asp Trp Trp Tyr Gly Ser Ile Gly Lys Gly Gln Glu
 260 265 270

Gly Tyr Phe Pro Ala Asn His Val Ala Ser Glu Thr Leu Tyr Gln Glu
 275 280 285

Leu Pro Pro Glu Ile Lys Glu Arg Ser Pro Pro Leu Ser Pro Glu Glu
 290 295 300

Lys Thr Lys Ile Glu Lys Ser Pro Ala Pro Gln Lys Val Lys
 305 310 315

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCCACCTA CACACCCAGC TCCCACCCAT GGAGAGCACC CCAGTCCTGT TCCTCCTGCC 60
 CTGGACCCTG GCCAACTCTG CCACAAGCTC TACCCTCGGT ACAACAGGCT CTGTCCCCAC 120
 ATCTACAGAC CCTGCCCCAT CTGCACACCT AGACTCAGTT CATAAGTCCA CAGACTCTGG 180
 CCCTTCAGAA CTGCCAGGCC CCACTCACAC CACTACAGGC TCTACCTATA GTGCCATTAC 240

CACTACCCAC AGTGCTCCAA GCCCCCTCAC TCACACTACT ACAGGCTCCA CCCACAAGCC 300
 CATAATCTCT ACCCTTACTA CTACAGGCCC TACCCTCAAT ATCATAGGCC CAGTCCAGAC 360
 TAGGACAAGC CCGACCEACA GTATGGCAAG GCTTACCCAT ACCACAGCAA GCCCCACTCA 420
 TACTTCCACA AGCCCCACCC ATACCCCCAC AAGTCCCACC CACAAAACCA GTATGTCACC 480
 TCCCACCACT ACAAGTCCTA CCCCCAGTGG TATGGGCCTA GTCCAGACTG CCACAAGTCC 540
 CACCCATCCT ACCACAAGCC CCACCCATCC CACCACAAGC CCCATCCTTA TAAATGTAAG 600
 CCCTTCCACT TCTCTAGAAC TTGCTACCTT CTCCAGCCCC TCCAAACACT CAGACCCAC 660
 CCTCCCAGGC ACTGACTCCC TTCCCTGTAG TCCCCAGTC TCCAATTCCT AACTCAGGC 720
 AGACCCATG GCCCCAGAA CTCCCCACCC AAGTCCTGCC CATTCCAGTA GGAAACCCCT 780
 CACAAGCCCT GCCCCAGATC CCTCAGAGTC TACGGTTCAG AGCTTAAGCC CCACTCCCTC 840
 ACCCCCAACC CCGCACCCC AGCATTCAGA CCTTTGCCCTG GCCATGGCTG TCCAGACCCC 900
 AGTCCCAACG GCAGCCGGAG GGTCTGGGGA CAGGAGCCTG GAGGAGGCAC TGGGGGCCCT 960
 AATGGCTGCC CTGGATGACT ACCGTGGCCA GTTTCCTGAG CTGCAGGGCC TGGAGCAGGA 1020
 GGTGACCCGC CTAGAAAGTC TGCTCATGCA GAGACAAGGT CTGACTCGCA GCCGGGCCTC 1080
 CAGTCTCAGC ATCACTGTGG AGCATGCCTT GGAGAGCTTC AGCTTCCTCA ATGAAAACGA 1140
 AGATGAAGAC AATGATGTTT CTGGGGACAG GCCTCCAAGC AGCCCGGAGG CTGGGGCTGA 1200
 GGACAGCATA GACTCACCCA GTGCCCCGCC CCTCAGCAGC GGGTGTCCAG CTCTGGATGC 1260
 TGCCTTGGTC CGGCACCTGT ACCACTGCAG TCGCCTCCTG CTGAAACTGG GCACATTTGG 1320
 GCCCCTGCGC TGCCAGGAGG CATGGGCCCT GGAGCGGCTG CTGCGGGAAG CCCGAGTACT 1380
 GGAGGCAGTA TGCGAGTTCA GCAGGCGGTG GGAGATCCCG GCCAGCTCTG CCCAGGAAGT 1440
 GGTGCAGTTC TCGCCTCTC GGCCTGGCTT CCTGACCTTC TGGGACCAGT GCACAGAGAG 1500
 ACTCAGCTGC TTCTCTGCG CCGTGGAGCG GGTGCTTCTC ACCTTCTGCA ACCAGTATGG 1560
 TGCCCGCCTC TCCCTGCGCC AGCCAGGCTT GGCTGAGGCT GTGTGTGTGA AGTTCCTGGA 1620
 GGATGCCCTG GGGCAGAAGC TGCCCAGAAG GCCCCAGCCA GGGCCTGGAG AGCAGCTCAC 1680
 AGTCTTCCAG TTCTGGAGTT TTGTGGAAC CTTGGACAGC CCCACCATGG AGGCCTACGT 1740
 GACTGAGACC GCTGAGGAGG TGCTACTGGT GCGGAATCTG AACTCGGATG ATCAGGCTGT 1800
 TGTGCTGAAG GCCCTGAGAT TGGCGCCCGA GGGGCGTCTG CGAAGGGACG GGCTGCGGGC 1860
 CCTCAGCTCC CTGCTCGTCC ATGGCAACAA CAAGGTCATG GCTGCTGTCA GCACCCAGCT 1920

```

CCGGAGCCTG TCACTGGGCC CTACCTTCCG GGAGAGGGCC CTCCTGTGCT TCCTGGACCA   1980
GCTGGAGGAT GAGGACGTGC AGACTCGAGT GGCTGGCTGC CTGGCCCTAG GCTGCATCAA   2040
GGCTGGCCGAG GGCATTGAGC CCCTGGTCTA CTCCTGCCAA ACTGACACAG AAGCTGTGAG   2100
GGAAGCTGCC CGGCAAAGCC TACAGCAGTG TGGAGAAGAG GGACAGTCTG CCCATCGACG   2160
GCTGGAGGAG TCCCTGGACG CCCTGCCCCG CATCTTTGGG CCTGGCAGCA TGGCCAGCAC   2220
AGCATTCTAA ACTATTACAC CATGGGTTCC TGGTGGCCCT TCCCCCCCAC TTTCAGGGCT   2280
CACCAGGCAC TGGCAGGGAG GGTAAGGGCT GGCTCCAGAT ACCCCTCCCC CACAGATTCC   2340
TAGCAATGAA AATCTAATAT ATTCTTCTGT TGCCCCTGGG GTTGGAGAGT CAGTGCCTGC   2400
AGTCAAGTGC CTCCCAGCCT CGGCTCAGCA CATCCCTTGC CACAAATCAG TGTCTGGGGC   2460
TTGGCCACCC TGCCGCTGCC CAGCCACATC CCTTGGTTTT GTATTTTATT TACAGAGTTT   2520
TACAGAAAAT AAAAAAGCAA AATGTCTTTC CTAAAAAAA AAAAAAA   2567

```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Met Glu Ser Thr Pro Val Leu Phe Leu Leu Pro Trp Thr Leu Ala Asn
1           5           10           15

```

```

Ser Ala Thr Ser Ser Thr Leu Gly Thr Thr Gly Ser Val Pro Thr Ser
20           25           30

```

```

Thr Asp Pro Ala Pro Ser Ala His Leu Asp Ser Val His Lys Ser Thr
35           40           45

```

```

Asp Ser Gly Pro Ser Glu Leu Pro Gly Pro Thr His Thr Thr Thr Gly
50           55           60

```

```

Ser Thr Tyr Ser Ala Ile Thr Thr Thr His Ser Ala Pro Ser Pro Leu
65           70           75           80

```

```

Thr His Thr Thr Thr Gly Ser Thr His Lys Pro Ile Ile Ser Thr Leu
85           90           95           100

```

Thr Thr Thr Gly Pro Thr Leu Asn Ile Ile Gly Pro Val Gln Thr Thr
 100 105 110

Thr Ser Pro Thr His Thr Met Pro Ser Pro Thr His Thr Thr Ala Ser
 115 120 125

Pro Thr His Thr Ser Thr Ser Pro Thr His Thr Pro Thr Ser Pro Thr
 130 135 140

His Lys Thr Ser Met Ser Pro Pro Thr Thr Thr Ser Pro Thr Pro Ser
 145 150 155 160

Gly Met Gly Leu Val Gln Thr Ala Thr Ser Pro Thr His Pro Thr Thr
 165 170 175

Ser Pro Thr His Pro Thr Thr Ser Pro Ile Leu Ile Asn Val Ser Pro
 180 185 190

Ser Thr Ser Leu Glu Leu Ala Thr Leu Ser Ser Pro Ser Lys His Ser
 195 200 205

Asp Pro Thr Leu Pro Gly Thr Asp Ser Leu Pro Cys Ser Pro Pro Val
 210 215 220

Ser Asn Ser Tyr Thr Gln Ala Asp Pro Met Ala Pro Arg Thr Pro His
 225 230 235 240

Pro Ser Pro Ala His Ser Ser Arg Lys Pro Leu Thr Ser Pro Ala Pro
 245 250 255

Asp Pro Ser Glu Ser Thr Val Gln Ser Leu Ser Pro Thr Pro Ser Pro
 260 265 270

Pro Thr Pro Ala Pro Gln His Ser Asp Leu Cys Leu Ala Met Ala Val
 275 280 285

Gln Thr Pro Val Pro Thr Ala Ala Gly Gly Ser Gly Asp Arg Ser Leu
 290 295 300

Glu Glu Ala Leu Gly Ala Leu Met Ala Ala Leu Asp Asp Tyr Arg Gly
 305 310 315 320

Gln Phe Pro Glu Leu Gln Gly Leu Glu Gln Glu Val Thr Arg Leu Glu
 325 330 335

Ser Leu Leu Met Gln Arg Gln Gly Leu Thr Arg Ser Arg Ala Ser Ser
 340 345 350

Leu Ser Ile Thr Val Glu His Ala Leu Glu Ser Phe Ser Phe Leu Asn
 355 360 365

Glu Asn Glu Asp Glu Asp Asn Asp Val Pro Gly Asp Arg Pro Pro Ser
 370 375 380

Ser Pro Glu Ala Gly Ala Glu Asp Ser Ile Asp Ser Pro Ser Ala Arg

385		390		395		400									
Pro	Leu	Ser	Thr	Gly	Cys	Pro	Ala	Leu	Asp	Ala	Ala	Leu	Val	Arg	His
				405					410					415	
Leu	Tyr	His	Cys	Ser	Arg	Leu	Leu	Leu	Lys	Leu	Gly	Thr	Phe	Gly	Pro
				420					425					430	
Leu	Arg	Cys	Gln	Glu	Ala	Trp	Ala	Leu	Glu	Arg	Leu	Leu	Arg	Glu	Ala
		435						440					445		
Arg	Val	Leu	Glu	Ala	Val	Cys	Glu	Phe	Ser	Arg	Arg	Trp	Glu	Ile	Pro
	450					455					460				
Ala	Ser	Ser	Ala	Gln	Glu	Val	Val	Gln	Phe	Ser	Ala	Ser	Arg	Pro	Gly
465					470					475					480
Phe	Leu	Thr	Phe	Trp	Asp	Gln	Cys	Thr	Glu	Arg	Leu	Ser	Cys	Phe	Leu
				485					490					495	
Cys	Pro	Val	Glu	Arg	Val	Leu	Leu	Thr	Phe	Cys	Asn	Gln	Tyr	Gly	Ala
			500					505					510		
Arg	Leu	Ser	Leu	Arg	Gln	Pro	Gly	Leu	Ala	Glu	Ala	Val	Cys	Val	Lys
	515					520						525			
Phe	Leu	Glu	Asp	Ala	Leu	Gly	Gln	Lys	Leu	Pro	Arg	Arg	Pro	Gln	Pro
	530					535					540				
Gly	Pro	Gly	Glu	Gln	Leu	Thr	Val	Phe	Gln	Phe	Trp	Ser	Phe	Val	Glu
545					550					555					560
Thr	Leu	Asp	Ser	Pro	Thr	Met	Glu	Ala	Tyr	Val	Thr	Glu	Thr	Ala	Glu
				565					570					575	
Glu	Val	Leu	Leu	Val	Arg	Asn	Leu	Asn	Ser	Asp	Asp	Gln	Ala	Val	Val
		580						585					590		
Leu	Lys	Ala	Leu	Arg	Leu	Ala	Pro	Glu	Gly	Arg	Leu	Arg	Arg	Asp	Gly
		595				600						605			
Leu	Arg	Ala	Leu	Ser	Ser	Leu	Leu	Val	His	Gly	Asn	Asn	Lys	Val	Met
	610					615					620				
Ala	Ala	Val	Ser	Thr	Gln	Leu	Arg	Ser	Leu	Ser	Leu	Gly	Pro	Thr	Phe
625					630					635					640
Arg	Glu	Arg	Ala	Leu	Leu	Cys	Phe	Leu	Asp	Gln	Leu	Glu	Asp	Glu	Asp
				645					650					655	
Val	Gln	Thr	Arg	Val	Ala	Gly	Cys	Leu	Ala	Leu	Gly	Cys	Ile	Lys	Ala
			660					665					670		
Pro	Glu	Gly	Ile	Glu	Pro	Leu	Val	Tyr	Leu	Cys	Gln	Thr	Asp	Thr	Glu
	675					680							685		

Ala Val Arg Glu Ala Ala Arg Gln Ser Leu Gln Gln Cys Gly Glu Glu
690 695 700

Gly Gln Ser Ala His Arg Arg Leu Glu Glu Ser Leu Asp Ala Leu Pro
705 710 715 720

Arg Ile Phe Gly Pro Gly Ser Met Ala Ser Thr Ala Phe
725 730

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

GGCAGTCAAA GCACTGATGA TGATAAAATC GTTCAGTACC ATTGGGAAGA ACTTAAGGGG      60
CCTCTAAGAG AAGAGAAGAT TTCTGAAGAT ACAGCCATAT TAAAACTAAG TAAACTCGTC      120
CCTGGGAACT ACACTTTCAG CTTGACTGTA GTAGACTCTG ATGGAGCTAC CAACTCTACT      180
ACTGCAAACC TGACAGTGAA CAAAGCTGTG GATTACCCCC CTGTGGCCAA CGCAGGCCCC      240
AACCAAGTGA TCACCCTGCC CCAAACTCC ATCACCTCTT TTGGGAACCA GAGCACTGAT      300
GATCATGGCA TCACCAGCTA TGAGTGGTCA CTCAGCCCAA GCAGCAAAGG GAAAGTGGTG      360
GAGATGCAGG GTGTTAGAAC ACCAACCTTA CAGCTCTCTG CGATGCAAGA AGGAGACTAC      420
ACTTACCAGC TCACAGTGAC TGACACAATA GGACAGCAGG CCACTGCTCA AGTGACTGTT      480
ATTGTGCAAC CTGAAAACAA TAAGCCTCCT CAGGCAGATG CAGGCCCAGA TAAAGAGCTG      540
ACCCCTCCTG TGGATAGCAC AACCTGGAT GGCAGCAAGA GCTCAGATGA TCAGAAAATT      600
ATCTCATATC TCTGGGAAAA AACACAGGGA CCTGATGGGG TGCAGCTCGA GAATGCTAAC      660
AGCAGTGTG CTA CTGTGAC TGGGCTGCAA GTGGGGACCT ATGTGTTTAC CTTGACTGTC      720
AAAGATGAGA GGAACCTGCA AAGCCAGAGC TCTGTGAATG TCATTGTCAA AGAAGAATAA      780
ACAAACCACC TATAGCCAAG ATAACTGGGA ATGTGGTGAT TACCCTACCC ACGAGCACAG      840
CAGAGCTGGA TGGCTCTAAG TCCTCAGATG ACAAGGGAAT AGTCAGCTAC CTCTGGACTC      900
GAGATGAGGG GAGCCCAGCA GCAGGGGAGG TGTAAATCA CTCTGACCAT CACCCTATCC      960

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TTTTCTTTT AAACCTGGTT GAGGGAACCT ACACTTTTC CCTGAAAGTG ACCGATGCAA 1020
AGGGTGAGAG TGACACAGAC CGGACCACTG TGGAGGTGAA ACCTGATCCC AGGAAAAACA 1080
ACCTGGTGGA GATCATCTTG GATATCAACG TCAGTCAGCT AACTGAGAGG CTGAAGGGGA 1140
TGTTCATCCG CCAGATTGGG GTCCTCCTGG GGGTGCTGGA TTCCGACATC ATTGTGCAAA 1200
AGATTCAGCC GTACACGGAG CAGAGCACCA AAATGGTATT TTTTGTTCAA AACGAGCCTC 1260
CCCACCAGAT CTTCAAAGGC CATGAGGTGG CAGCGATGCT CAAGAGTGAG CTGCGGAAGC 1320
AAAAGGCAGA CTTTTTGATA TTCAGAGCCT TGGAAGTCAA CACTGTCACA TGTCAGCTGA 1380
ACTGTTCCGA CCATGGCTAC TGTGACTCGT TCACCAAACG CTGTATCTGT GACCCTTTTTT 1440
GGATGGAGAA TTTCATCAAG GTGCAGCTGA GGGATGGAGA CAGCAACTGT GAGTGGAGCG 1500
TGTTATATGT TATCATTGCT ACCTTTGTCA TTGTTGTTGC CTTGGGAATC CTGTCTTGGA 1560
CTGTGATCTG TTGTTGTAAG AGGCAAAAAG GAAAACCCAA GAGGAAAAGC AAGTACAAGA 1620
TCTGGATGCC ACGGATCAGG AAAGCTTGGA GCTGAAGCCA ACCTCCCGAG CAGGCATCAA 1680
ACAGAAAGGC CTTTTGCTAA GTAGCAGCCT GATGCACTCC GAGTCAGAGC TGGACAGCGA 1740
TGATGCCATC TTTACATGGC CAGACCGAGA GAAGGGCAAA CTCCTGCATG GTCAGAATGG 1800
CTCTGTACCC AACGGGCAGA CCCCTCTGAA GGCCAGGAGC CCGCGGGAGG AGATCCTGTA 1860
GCCACCTGGT CTGTCTCCTC AGGGCAGGGC CCAGCACACT GCCC GCCAG TCCTCCTACC 1920
TCCCGAGTCT GCGGGCAGCT GCTGTCCCAG CATCTGCTGG TCATTTCGCC CTGACAGTCC 1980
CAACCAGAAC CCCTGGGACT TGAATCCAGA GACGTCTTTC AGGAACCCCT CAACGAAGCT 2040
GTGAATGAAG AGGTTTCCTC TTAAACCTG TCTGGTGGGC CCCCAGATAT CCTCACCTCA 2100
GGGCCTCCTT TTTTGTGAAA CTCCTCCCCT CCCCCGAGG CAGACCCAGC CAGCTGCTAA 2160
GCTCTGCAGC TCCCCAGTGG ACAGTGTCAT TGTGCCCAGA GTGCTGCAAG GTGAGGCCTG 2220
CTGTGCTGCC CGCACACCTG AGTGCAAAAC CAAGCACTGT GGGCATGGTG TTTCCCTCTC 2280
TGGGGTAGAG TACGCCCTCT CGCTGGGCAA AGAGGAAGTG GCACCCCTCC CCTCACCACA 2340
GATGCTGAGA TGGTAGCATA GAAATGATGG CCGGGCGCGG TGGCTMACGC CTGTAATCCC 2400
AGCACTTTGG GAGGCCGAGG CGGGCGGATC ATGAGGTCAG GAGATCAAGA CCACCTGGC 2460
TAACACGGTG AAACCCCATC TCTACTAAAA AAAAAAAAAA A 2501

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Gln Gly Val Arg Thr Pro Thr Leu Gln Leu Ser Ala Met Gln Glu
1           5           10           15

Gly Asp Tyr Thr Tyr Gln Leu Thr Val Thr Asp Thr Ile Gly Gln Gln
                20           25           30

Ala Thr Ala Gln Val Thr Val Ile Val Gln Pro Glu Asn Asn Lys Pro
          35           40           45

Pro Gln Ala Asp Ala Gly Pro Asp Lys Glu Leu Thr Leu Pro Val Asp
          50           55           60

Ser Thr Thr Leu Asp Gly Ser Lys Ser Ser Asp Asp Gln Lys Ile Ile
65           70           75           80

Ser Tyr Leu Trp Glu Lys Thr Gln Gly Pro Asp Gly Val Gln Leu Glu
          85           90           95

Asn Ala Asn Ser Ser Val Ala Thr Val Thr Gly Leu Gln Val Gly Thr
          100          105          110

Tyr Val Phe Thr Leu Thr Val Lys Asp Glu Arg Asn Leu Gln Ser Gln
          115          120          125

Ser Ser Val Asn Val Ile Val Lys Glu Glu
          130          135

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1820 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

 GGCAGCAGCA GAGGGAGAGC TCGGGGCTTG GAGGGGAAAC AGCGGAAGAC CTAAGATTAT 60

CGGGAGGGCA GCAGAGGCAG AGAACGAGGA CAGGACCCCTT GGCCGTCTTC TTCCAGGGAA 120
 CGAGAGGTCA CAGCCTCGCT CTCCGCTTAG GCTTCTGGCG CCCAGCTTA AAGCCGAGGC 180
 TCGCGCTGAC AAAGGGCTCG CGCCGGTGCC GCCGCCCTTC TCATCCGGGC ATTCGGGTCC 240
 CTGCGGAGAG GGAGGGGGAA GGGCAGAGGG GGAGGGGAAG GAGCCSGAGG GGCSCACACT 300
 TGGAGCTGAA GCCCTCTCCA GGGCTCCGGG CCGGTGCCCC AACGGACAGA GGTGAGGAG 360
 GACCCGCAGA GGTGGCAGCG GCCGGGGGCA GGAGGATGGT GCAGAAGGAG AGTCAAGCGA 420
 CGTTGGAGGA GCGGGAGAGC GAGCTCAGTT CCAACCCTGC CGCCTCTGCG GGGGCATCGC 480
 TGGAGCCGCC GGCAGCTCCG GCACCCGAG AAGACAACCC CGCCGGGGCT GGGGGAGCGG 540
 CGGTGGCCGG GGCTGCAGGA GGGGCTCGGC GGTTCCTCT GCGGTGTGGT GGAAGGATTT 600
 TATGGAAGAC CTTGGGTAT GGAACAGAGA AAAGAACTCT TTAGAAGGCT CCAGAAATGG 660
 GAATTAAATA CATACTTGTA TGCCCCAAAA GATGACTACA AACATAGGAT GTTTTGCGA 720
 GAGATGTATT CAGTGGAGGA AGCTGAGCAA CTTATGACTC TCATCTCTGC TGCACGAGAA 780
 TATGAGATAG AGTTCATCTA TGCGATCTCA CCTGGATTGG ATATCACTTT TTCTAACCCC 840
 AAGGAAGTAT CCACATTGAA ACGTAAATG GACCAGGTTT CTCAGTTTGG GTGCAGATCA 900
 TTTGCTTTGC TTTTGTATGA TATAGACCAT AATATGTGTG CAGCAGACAA AGAGGTATTC 960
 AGTTCTTTTG CTCATGCCCC AGTCTCCATC ACAAATGAAA TCTATCAGTA CCTAGGAGAG 1020
 CCAGAAACTT TCCTCTTCTG TCCCACAGAA TACTGTGGCA CTTTCTGTTA TCCAAATGTG 1080
 TCTCAGTCTC CATATTTAAG GACTGTGGGT GAAAAGCTTC TACCTGGAAT TGAAGTGCTT 1140
 TGGACAGGTC CCAAAGTTGT TTCTAAAGAA ATTCCAGTAG AGTCCATCGA AGAGGTTTCT 1200
 AAGATTATTA AGAGAGCTCC AGTAATCTGG GATAACATTC ATGCTAATGA TTATGATCAG 1260
 AAGAGACTGT TTCTGGGCCC GTACAAAGGA AGATCCACAG AACTCATCCC ACGGTAAAA 1320
 GGAGTCCTCA CTAATCCAAA TTGTGAATTT GAAGCCAACT ACGTTGCTAT CCACACCCTT 1380
 GCCACCTGGT ACAAATCAAA CATGAATGGG AGTGAGAAAA GATGTAGTGA TGAAGTACAG 1440
 TGAAGATAGT ACTGTGTCCA TCCAGATAAA ATTAGAAAAT GAAGGCAGTG ATGAAGATAT 1500
 TGAAGCTGAT GTAATCTATA GTCCACAGAT GGCTCTAAAG CTAGCATTA CAGAATGGTT 1560
 GCAAGAGTTT GGTGTGCTC ATCAATACAG CAGTAGGCAA GTTGACACA GTGGAGCTAA 1620
 AGCAAGTGTA GTTGATGGGA CTCCTTTAGT TGCAGCACC TCTTAAATG CCACAACCGT 1680
 AGTAACAACA GTTTATCAGG AGCCATTAT GAGCCAGGGA GCAGCCTTGA GTGGTGAGCC 1740

TACTACTCTG ACCAAGGAAG AAGAAAAGAA ACAGCCTGAT GAAGAACCCA TGGACATGGT 1800
GGTGGAAGAAA AAAAAAAAAA 1820

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Glu Gln Arg Lys Glu Leu Phe Arg Arg Leu Gln Lys Trp Glu Leu
1 5 10 15

Asn Thr Tyr Leu Tyr Ala Pro Lys Asp Asp Tyr Lys His Arg Met Phe
20 25 30

Trp Arg Glu Met Tyr Ser Val Glu Glu Ala Glu Gln Leu Met Thr Leu
35 40 45

Ile Ser Ala Ala Arg Glu Tyr Glu Ile Glu Phe Ile Tyr Ala Ile Ser
50 55 60

Pro Gly Leu Asp Ile Thr Phe Ser Asn Pro Lys Glu Val Ser Thr Leu
65 70 75 80

Lys Arg Lys Leu Asp Gln Val Ser Gln Phe Gly Cys Arg Ser Phe Ala
85 90 95

Leu Leu Phe Asp Asp Ile Asp His Asn Met Cys Ala Ala Asp Lys Glu
100 105 110

Val Phe Ser Ser Phe Ala His Ala Gln Val Ser Ile Thr Asn Glu Ile
115 120 125

Tyr Gln Tyr Leu Gly Glu Pro Glu Thr Phe Leu Phe Cys Pro Thr Glu
130 135 140

Tyr Cys Gly Thr Phe Cys Tyr Pro Asn Val Ser Gln Ser Pro Tyr Leu
145 150 155 160

Arg Thr Val Gly Glu Lys Leu Leu Pro Gly Ile Glu Val Leu Trp Thr
165 170 175

Gly Pro Lys Val Val Ser Lys Glu Ile Pro Val Glu Ser Ile Glu Glu
180 185 190

Val Ser Lys Ile Ile Lys Arg Ala Pro Val Ile Trp Asp Asn Ile His
 195 200 205

Ala Asn Asp Tyr Asp Gln Lys Arg Leu Phe Leu Gly Pro Tyr Lys Gly
 210 215 220

Arg Ser Thr Glu Leu Ile Pro Arg Leu Lys Gly Val Leu Thr Asn Pro

225 230 235 240

Asn Cys Glu Phe Glu Ala Asn Tyr Val Ala Ile His Thr Leu Ala Thr
 245 250 255

Trp Tyr Lys Ser Asn Met Asn Gly Ser Glu Lys Arg Cys Ser Asp Asp
 260 265 270

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TATCCATTAC GTCGACTAAT ACGTACATAA GAATTCAATC GGGAGACAAT GTAATAACCC 60
 AAACACTGGG TATTCATATT TGACACATGG GCAAACCTGC CAGTGAATG GAATTGTGAC 120
 CTGACAGAGA AGGGAAGGCA GGCTGACGAA GGTGATCGAA TGGGAGAACA GTGCTGTGGT 180
 GATCATGAGA ATGAGGCTTT TCTGTAGCAT GTAAACCAA CCGGACCCCTT GGCAGTTCGT 240
 CGTCCCTCAG TTCTCCAGAT GCTATTTTTT GCAGGTTCTA CCAAGTGCTT GTTGATTACC 300
 CTAGTTGTAA TTATCTAGGG AAGAGATGAA TGTAAGTGAG AGTGCAGAGC ACTGGGGAGG 360
 GTGACAGTGA AATGCAATTA GAGGCAGCAA GAGAGTCCTA GTCTGTTCTC ACATAACCGG 420
 ACTTGAACGC TCCAGTGCGA GCAGAGTGCT GGGGGTGGAT TCCACTGCCG AACCACGGCA 480
 GCTTTGCTTT ACTCTTCAGC ATGGGGGTGG TAACTAGCTG CACAGCAAGT TATGAAATGG 540
 AAAGCAAGCT TAACAGCTGT AATCTCATCG GATACCCTGG AGCAAATGCC TTGGGATTGC 600
 CTGAAGTGAA GTGTTTAGCA TCCACCAAAT AGTTGAGTTT CTAAGATGGG CCATGCGGGA 660
 TCCCTGCCAC ACGGGTGTGG GGGCAGCGCG CTCTTCCTG GGTGGGTGC TGTGGTCTTA 720

AGTCTTCATG TTTCCCTTG GCGTCACCTC TGGTCCTGTC CATCTTGTGC ACATGTGTCC 780
 CTGAGGGCGA GTCACACCTG TGTCTTGAGT CTGCTGTAAG GTGTTCAAGT TACCTCAAGG 840
 GGTGATGATG GTAAGCTGTA TCGGACGGCA TCGTCCGTCC ATCACCACAC AACTGGAAT 900
 GTATCCCCC CGCCCTGCCC CTTGATAAC CTCCTGACCT TGTCTTTCCT ATAATCACCA 960
 CAACTCCTA GTGCAATTG GATGCTGCTT TAAATGTGAA AACAATTGTT CAAAAGCTAT 1020
 AAAACCTGAA TGAAAGCTGA AGCTGAATTT ATAAGCCTTG TTGCATATGA GCCAAAAGTG 1080
 CAAAAGCTC TATATAATGA ACTAACCTGC CACTCGTATA AATATAAATA TATATAAATA 1140
 TATTAAAATC AGACTGTTCT ACAAATTGT GTATTTGTAT TTTTGTGTAC GTACAATTTT 1200
 CTGCTAAGCA GAAGGAGGAT GTAGTATAGG ATGCTGTGAG AAGAGATTG GTTTAATCCT 1260
 ATTCTTTTGT TACTTATTTT TGTTAACATC AGATGCCTGT CTTTGTCTTA TATGTGTATG 1320
 AACTGTTTG GAAAGCTGCA GTATCTCTCT TCCTGAGGTC CAGAGGCCAT TAAAGAATAA 1380
 ACATGGGGCT TAGAGGTGTC TTGGCCACCA AACACAGGTA AGCCAACAGA GTTCGGCTCC 1440
 CGTACGTGGT GTGGTGGACC TGGGGCCTGG AGCCACTTGT ACTCCTGGGG TGGGACTGAG 1500
 GGAGGGAAAG GGCTCCCCCA CTTGAGGCTG GTCAGTGTAT GTTGACTTCC CTCTGGGAAG 1560
 CAAAATTCCA CTTGTAAAAA TCAGCTTCCA AGACAAAAGA TGATCCGATG TCACTTCTGG 1620
 GTCACCAGGA AGGGACACAG GATCTCTCTG AACTTTGGAA CAGACCCTCA TATTCTGGGG 1680
 CCAGAAGTTT GCCCAGAAAG CAGCAGGTGG CTCTGCCTGG CTGTAGAGCC CAGCTCATTG 1740
 GCTGTCCCTG GGCTTGGTCT CCCTCTTCCG AGTAGTTGCT GCCTTTCTTC AGATCAGGTT 1800
 ACCACAATGC CTCCCGCTG CTGACGCTTC ATCCCCACA CCTCCAGCCC CAGTTACCTG 1860
 GAGCTTCTCA GAACCCACTT TGCCGGTGCT AAAACACAAG AGGGGGTGAA AGTGGCTGCC 1920
 AGTAATGGCC AGAAACCAAC CACCAGAGGC CAGGCTGAAA GACAAGCTCC GGGTGTCCAG 1980
 GGGCTGACGG GCCAACCATG TGGCAGGTCC CAGGCCCCAC CCACTGCGCC ATCCGCCTCT 2040
 GAGCTCCACA GTGGTCCCAC TAATGGGAAC CTCCTCTAGG GAGAGTGATA CTGCACCTTC 2100
 ACCCGTAGGA CTCATATTTA TAACAATGTG TAATGGCTGT AGCAAAAAGC CCTGTGTTCT 2160
 AGATGTAAAT GGTCAAAGAA ACAAGCGCTC TATTGTTTTG AATAAAATAG TTCAAATGAG 2220
 TCCTGTATCA TTGTATCTCC TATTCTGGAT TAGTGCCTTT TGGACAGTAG ACTGTTCTGT 2280
 AATTAAATG TAGTATACTG CTTTTTGTG CAGTTTTGTT TTAATAAAAC TTTTTTTTAA 2340
 TTTGTGTTA TTTTAGTATT GTACCTATTA GAGAATAAAA TGTATAACTG AAAAAAAAAA 2400

AAAAA

2405

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Met Gly Thr Ser Ser Arg Glu Ser Asp Thr Ala Pro Ser Pro Val Gly
1             5             10             15

Leu Ile Phe Ile Thr Met Cys Asn Gly Cys Ser Lys Lys Pro Leu Phe
                20             25             30

Leu Asp Val Asn Gly Gln Arg Asn Lys Arg Ser Ile Val Leu Asn Lys
            35             40             45

Ile Val Gln Met Ser Pro Val Ser Leu Tyr Leu Leu Phe Trp Ile Ser
50             55             60

Ala Phe Trp Thr Val Asp Cys Ser Val Ile Lys Met
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CNAGCAGCAGA TACAGCAGTA AGGAAGGC

29

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid

10175272.051802

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

```
(A) DESCRIPTION: /desc= "oligonucleotide"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGGCTCTCCTT AATCGCCGTC TCAAACAT

29

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

```
(A) DESCRIPTION: /desc = "oligonucleotide"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CNTTGGCCAGG TCTTCCTGCT CCTTCATT

29

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

```
(A) DESCRIPTION: /desc = "oligonucleotide"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ANGCTGCAAAG CTGGTGTAGA AGTAGGTG

29

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

[illegible]

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

|||||

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ANTTAGCCATG TCACTCCGCA GGAAGTCC

29

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TNTAGTCATAA AGAGCCACTA CCGTTGGT

29

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TNGTATGGGTA GGGCTTGGCA TAGTGTGG

29

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

|||||

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

=====

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TNTCAGGTTTG CAGTAGTAGA GTTGGTAG

29

- (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CNTCTTCGATG GACTCTACTG GAATTTCT

29

- (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TNAGCCTGGCC TCTGGTGGTT GGTTCCTG

29

- (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

=====

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

1  Thr Leu Lys Leu Cys Ser Pro Pro Lys Asp His Glu Val Leu Gly Val
5  10  15
20  Ile Gln Arg Phe Leu Lys Leu Arg Ser Pro Trp Lys Ala Leu Ile Thr
25  30
35  Thr Ile Leu Lys Pro Gln Leu Phe Glu Pro Arg Pro Arg Leu Thr Val
40  45
50  Leu Thr Phe Pro Ser Ser His Glu Gly Glu Ser Phe Pro Leu Ala Trp
55  60
65  Asn Ala Lys Ile Thr Asp Leu Lys Gln Lys Val Glu Asn Leu Phe Asn
70  75  80
85  Glu Lys Cys Gly Glu Ala Leu Gly Leu Lys Gln Ala Val Lys Val Pro
90  95
100 Phe Ala Leu Phe Glu Ser Phe Pro Glu Asp Phe Tyr Val Glu Gly Leu
105  110
115 Pro Glu Gly Val Pro Phe Arg Arg Pro Ser Thr Phe Gly Ile Pro Arg
120  125
130 Leu Glu Lys Ile Leu Arg Asn Lys Ala Lys Ile Lys Phe Ile Ile Lys
135  140
145 Lys Pro Glu Met Phe Glu Thr Ala Ile Lys Glu Ser Thr Ser Ser Lys
150  155  160
165 Ser Pro Pro Arg Lys Ile Asn Ser Ser Pro Asn Val Asn Thr Thr Ala
170  175
180 Ser Gly Val Glu Asp Leu Asn Ile Ile Gln Val Thr Ile Pro Asp Asp
185  190
195 Asp Asn Glu Arg Leu Ser Lys Val Glu Lys Ala Arg Gln Leu Arg Glu
200  205
210 Gln Val Asn Asp Leu Phe Ser Arg Lys Phe Gly Glu Ala Ile Gly Met
215  220
225 Gly Phe Pro Val Lys Val Pro Tyr Arg Lys Ile Thr Ile Asn Pro Gly
230  235  240
245 Cys Val Val Val Asp Gly Met Pro Pro Gly Val Ser Phe Lys Ala Pro
250  255
260 Ser Tyr Leu Glu Ile Ser Ser Met Arg Arg Ile Leu Asp Ser Ala Thr
265  270

```

```

Phe Ile Lys Phe Thr Val Ile Arg Pro Phe Pro Gly Leu Val Ile Asn
      275                      280                      285

Asn Gln Leu Val Asp Gln Ser Glu Ser Lys Gly Pro Val Ile Gln Glu
      290                      295                      300
Ser Ala Glu Pro Ser Gln Leu Glu Val Pro Ala Thr Glu Glu Ile Lys
      305                      310                      315                      320
Glu Thr Asp Gly Ser Ser Gln Ile Lys Gln Glu Pro Asp Pro Thr Trp
      325                      330                      335

```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ANCTTGGCCA GGTCTTCCTG CTCCTTCAT

29

What is claimed is:

1. An isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID

NO:1

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID

NO:1 from nucleotide 521 to nucleotide 1111;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID

NO:1 from nucleotide 536 to nucleotide 817;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ax318_3 deposited under accession number ATCC 98353;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ax318_3 deposited under accession number ATCC 98353;

(f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone ax318_3 deposited under accession number ATCC 98353;

(g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone ax318_3 deposited under accession number ATCC 98353;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 93 to amino acid 102 of SEQ ID NO:2;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.

3. A host cell transformed with the polynucleotide of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:
 - (a) growing a culture of the host cell of claim 3 in a suitable culture medium; and
 - (b) purifying said protein from the culture.
6. A protein produced according to the process of claim 5.
7. The protein of claim 6 comprising a mature protein.
8. A protein comprising an amino acid sequence selected from the group consisting of:
 - (a) the amino acid sequence of SEQ ID NO:2;
 - (b) the amino acid sequence of SEQ ID NO:2 from amino acid 4 to amino acid 99;
 - (c) fragments of the amino acid sequence of SEQ ID NO:2 comprising the amino acid sequence from amino acid 93 to amino acid 102 of SEQ ID NO:2; and
 - (d) the amino acid sequence encoded by the cDNA insert of clone ax318_3 deposited under accession number ATCC 98353;the protein being substantially free from other mammalian proteins.
9. The protein of claim 8, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.
10. The protein of claim 8, wherein said protein comprises the amino acid sequence of SEQ ID NO:2 from amino acid 4 to amino acid 99.
11. A composition comprising the protein of claim 8 and a pharmaceutically acceptable carrier.

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12. A method for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition of claim 11.

~~13. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:1.~~

14. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 61 to nucleotide 864;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 826 to nucleotide 1386;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bg140_1 deposited under accession number ATCC 98353;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bg140_1 deposited under accession number ATCC 98353;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone bg140_1 deposited under accession number ATCC 98353;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone bg140_1 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:4;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

~~15. A method for preventing, treating or ameliorating a medical condition~~

(l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

15. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
- (b) the amino acid sequence of SEQ ID NO:31;
- (c) the amino acid sequence of SEQ ID NO:31 from amino acid 148 to amino acid 249;
- (d) fragments of the amino acid sequence of SEQ ID NO:4 comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:4;
- (e) fragments of the amino acid sequence of SEQ ID NO:31 comprising the amino acid sequence from amino acid 163 to amino acid 172 of SEQ ID NO:31;
- and
- (f) the amino acid sequence encoded by the cDNA insert of clone bg140_1 deposited under accession number ATCC 98353;

the protein being substantially free from other mammalian proteins.

16. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:3.

17. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 77 to nucleotide 1624;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 390 to nucleotide 789;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bg465_2 deposited under accession number ATCC 98353;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bg465_2 deposited under accession number ATCC 98353;

- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone bg465_2 deposited under accession number ATCC 98353;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone bg465_2 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 253 to amino acid 262 of SEQ ID NO:6;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

18. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
 - (b) the amino acid sequence of SEQ ID NO:6 from amino acid 260 to amino acid 343;
 - (c) fragments of the amino acid sequence of SEQ ID NO:6 comprising the amino acid sequence from amino acid 253 to amino acid 262 of SEQ ID NO:6; and
 - (d) the amino acid sequence encoded by the cDNA insert of clone bg465_2 deposited under accession number ATCC 98353;
- the protein being substantially free from other mammalian proteins.

19. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:5.

20. An isolated polynucleotide selected from the group consisting of:

11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 48 to nucleotide 1055;
- ~~(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 216 to nucleotide 1055;~~
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 494 to nucleotide 958;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bk291_3 deposited under accession number ATCC 98353;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bk291_3 deposited under accession number ATCC 98353;
- (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone bk291_3 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone bk291_3 deposited under accession number ATCC 98353;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 85 to amino acid 94 of SEQ ID NO:8;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

21. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;

- (b) the amino acid sequence of SEQ ID NO:8 from amino acid 188 to amino acid 306;
 - (c) fragments of the amino acid sequence of SEQ ID NO:8 comprising the amino acid sequence from amino acid 85 to amino acid 94 of SEQ ID NO:8; and
 - (d) the amino acid sequence encoded by the cDNA insert of clone bk291_3 deposited under accession number ATCC 98353;
- the protein being substantially free from other mammalian proteins.

22. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:7.

23. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 64 to nucleotide 1197;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 1 to nucleotide 828;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bp537_4 deposited under accession number ATCC 98353;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bp537_4 deposited under accession number ATCC 98353;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone bp537_4 deposited under accession number ATCC 98353;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone bp537_4 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:10;

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(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

~~(l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).~~

24. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:10;

(b) the amino acid sequence of SEQ ID NO:10 from amino acid 1 to amino acid 255;

(c) fragments of the amino acid sequence of SEQ ID NO:10 comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:10; and

(d) the amino acid sequence encoded by the cDNA insert of clone bp537_4 deposited under accession number ATCC 98353;

the protein being substantially free from other mammalian proteins.

25. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:9.

26. An isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 581 to nucleotide 1534;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 928 to nucleotide 1510;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cs431_2 deposited under accession number ATCC 98353;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cs431_2 deposited under accession number ATCC 98353;

~~(f) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(e).~~

- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone cs431_2 deposited under accession number ATCC 98353;
- (g) a polynucleotide encoding the mature protein encoded by the DNA insert of clone cs431_2 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 154 to amino acid 163 of SEQ ID NO:12;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

27. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
- (b) the amino acid sequence of SEQ ID NO:12 from amino acid 150 to amino acid 310;
- (c) fragments of the amino acid sequence of SEQ ID NO:12 comprising the amino acid sequence from amino acid 154 to amino acid 163 of SEQ ID NO:12;
- and
- (d) the amino acid sequence encoded by the cDNA insert of clone cs431_2 deposited under accession number ATCC 98353;
- the protein being substantially free from other mammalian proteins.

28. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:11.

29. An isolated polynucleotide selected from the group consisting of:

.. 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 29 to nucleotide 2227;
- ~~SEQ ID NO:13~~ (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 1334 to nucleotide 2227;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 1 to nucleotide 746;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw976_1 deposited under accession number ATCC 98353;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw976_1 deposited under accession number ATCC 98353;
- (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone cw976_1 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone cw976_1 deposited under accession number ATCC 98353;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 361 to amino acid 370 of SEQ ID NO:14;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

30. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14; ~~SEQ ID NO:14~~

- (b) the amino acid sequence of SEQ ID NO:14 from amino acid 1 to amino acid 239;
 - (c) the amino acid sequence of SEQ ID NO:14 from amino acid 119 to amino acid 733;
 - (d) fragments of the amino acid sequence of SEQ ID NO:14 comprising the amino acid sequence from amino acid 361 to amino acid 370 of SEQ ID NO:14; and
 - (e) the amino acid sequence encoded by the cDNA insert of clone cw976_1 deposited under accession number ATCC 98353;
- the protein being substantially free from other mammalian proteins.

31. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:13.

32. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 364 to nucleotide 777;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 1 to nucleotide 636;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1233_3 deposited under accession number ATCC 98353;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1233_3 deposited under accession number ATCC 98353;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone cw1233_3 deposited under accession number ATCC 98353;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone cw1233_3 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment

comprising the amino acid sequence from amino acid 64 to amino acid 73 of SEQ ID NO:16;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

~~(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and~~

(l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

33. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) the amino acid sequence of SEQ ID NO:16 from amino acid 1 to amino acid 91;

(c) fragments of the amino acid sequence of SEQ ID NO:16 comprising the amino acid sequence from amino acid 64 to amino acid 73 of SEQ ID NO:16; and

(d) the amino acid sequence encoded by the cDNA insert of clone cw1233_3 deposited under accession number ATCC 98353;

the protein being substantially free from other mammalian proteins.

34. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:15.

35. An isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 619 to nucleotide 1434;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 520 to nucleotide 1323;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dg1_1 deposited under accession number ATCC 98353;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dg1_1 deposited under accession number ATCC 98353;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone dg1_1 deposited under accession number ATCC 98353;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone dg1_1 deposited under accession number ATCC 98353;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 131 to amino acid 140 of SEQ ID NO:18;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

36. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
- (b) the amino acid sequence of SEQ ID NO:18 from amino acid 1 to amino acid 235;
- (c) fragments of the amino acid sequence of SEQ ID NO:18 comprising the amino acid sequence from amino acid 131 to amino acid 140 of SEQ ID NO:18; and
- (d) the amino acid sequence encoded by the cDNA insert of clone dg1_1 deposited under accession number ATCC 98353;

the protein being substantially free from other mammalian proteins.

37. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:17.

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38. An isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 2063 to nucleotide 2290;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 2276 to nucleotide 2290;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 2037 to nucleotide 2405;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ep234_1 deposited under accession number ATCC 98353;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ep234_1 deposited under accession number ATCC 98353;

(g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone ep234_1 deposited under accession number ATCC 98353;

(h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone ep234_1 deposited under accession number ATCC 98353;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:20;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and

(m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

39. A protein comprising an amino acid sequence selected from the group consisting of:

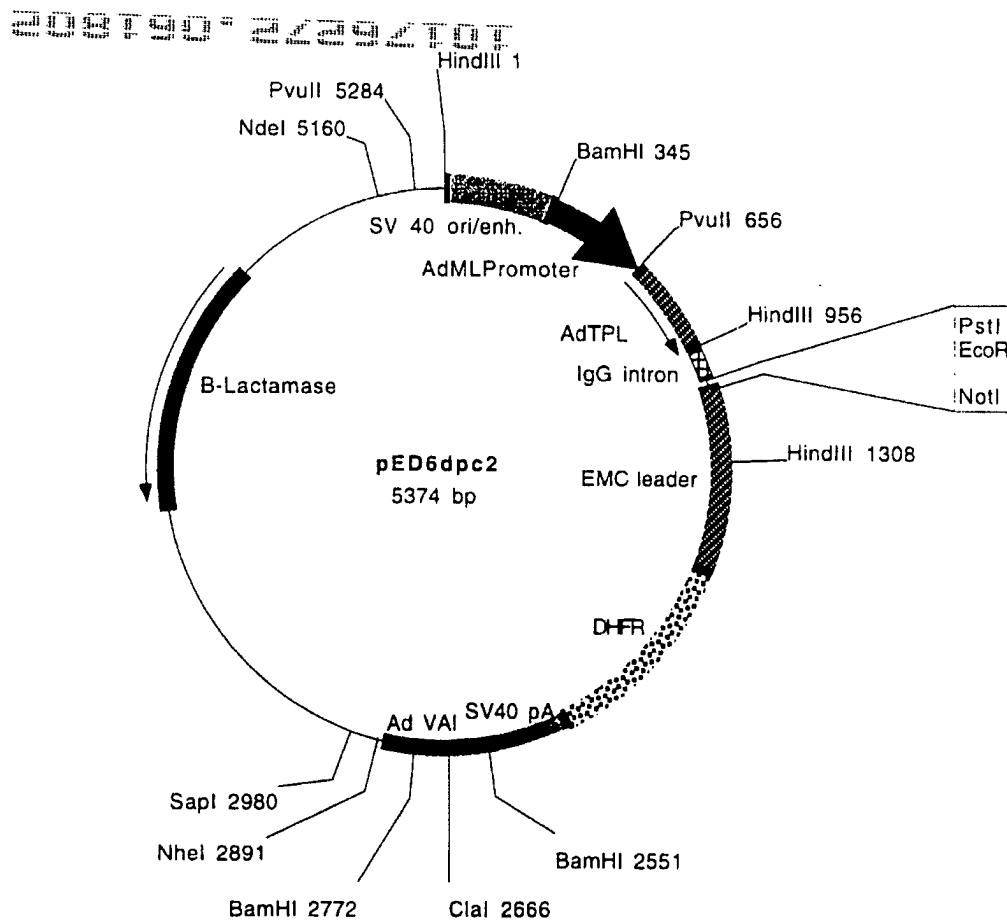
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 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- (a) the amino acid sequence of SEQ ID NO:20;
 - (b) the amino acid sequence of SEQ ID NO:20 from amino acid 1 to amino acid 69;
 - (c) fragments of the amino acid sequence of SEQ ID NO:20 comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:20;
and
 - (d) the amino acid sequence encoded by the cDNA insert of clone ep234_1 deposited under accession number ATCC 98353;
- the protein being substantially free from other mammalian proteins.

40. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:19.

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FIGURE 1A

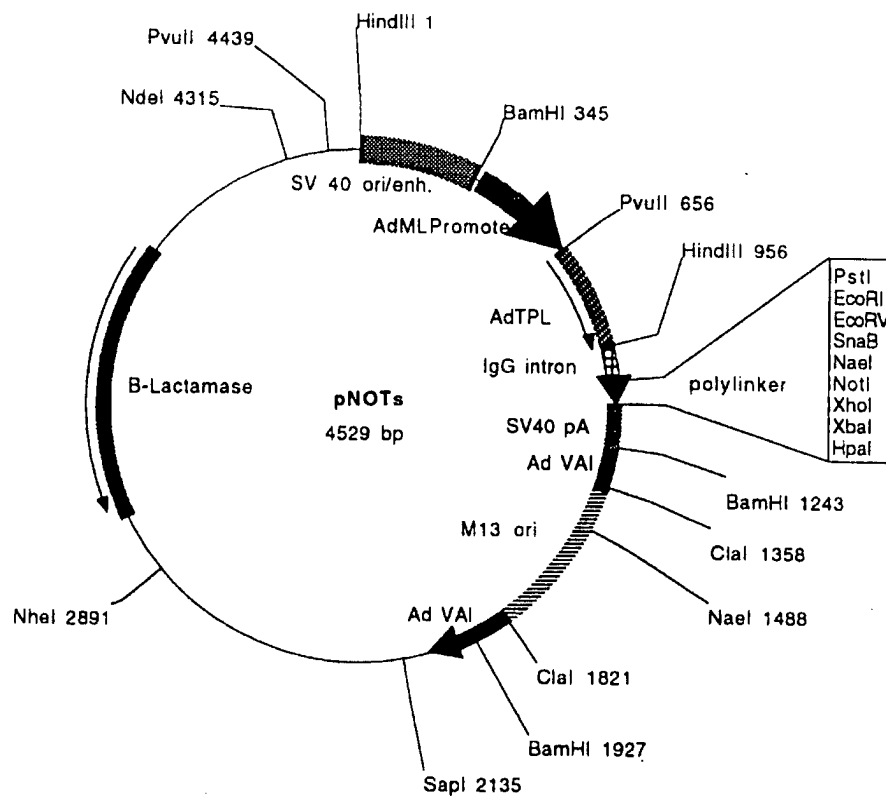


Plasmid name: pED6dpc2

Plasmid size: 5374 bp

Comments/References: pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

FIGURE 1B



Plasmid name: pNOTs

Plasmid size: 4529 bp

Comments/References: pNOTs is a derivative of pMT2 (Kaufman et al, 1989. Mol. Cell. Biol. 9:1741-1750). DHFR was deleted and a new polylinker was inserted between EcoRI and HpaI. M13 origin of replication was inserted in the Clal site. SST cDNAs are cloned between EcoRI and NotI